

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:34:20 ; Search time 91.4571 Seconds
(without alignments)
558.211 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

Sequence: 1 SYMTINNFSCREEMGEVI.....EANGLLPDKLTLFCEVSVV 132

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_16Dec04:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	132	4	Aae03669 Human SPO
2	132	100.0	180	4	Aae03662 Human SPO
3	132	100.0	374	4	Aab90799 Human she
4	132	100.0	374	4	Aae03659 Human SPO
5	132	100.0	374	7	Adb85287 Human pro
6	132	100.0	374	7	Adi62718 Human apo
7	132	100.0	374	8	Adg89936 Antagonis
8	132	100.0	374	8	Adg89928 Antagonis
9	132	100.0	385	3	Abs58286 Lung canc
10	63	47.7	398	4	ABG23713 Novel hum
11	53	40.2	391	4	ABAB94987
12	53	40.2	391	8	AQD89926
13	53	40.2	391	8	AQD89934
14	53	40.2	392	5	ABP43818
15	53	40.2	392	6	ABU96687
16	40	30.3	377	4	ABB64759
17	40	30.3	377	8	ADSG6756
18	35	26.5	35	4	ABB40093
19	35	26.5	35	4	AAM33727
20	35	26.5	35	4	AAM73533
21	35	26.5	35	4	AAM60850
22	35	26.5	35	4	ABG55260
23	35	26.5	35	5	ABG43394
24	33	25.0	195	4	AAU16237
25	33	25.0	195	6	ABU55306

AbB84635 S. aureus
Adf09194 S. aureus
Adh39727 Streptomy
Aam87295 Human km
Adf59258 Human PDI
Abu11487 Human MDD
Abu11676 Human MDD
Aag12069 Arabidops
Aag12068 Arabidops
Aag15516 Arabidops
Aad27321 B. napus
Aab27319 B. napus
Aab27320 B. napus
Aga54812 Human pro
Aga54811 Arabidops
Adb89576 Human pol
Adu39486 Protein e
Adal3323 Human int
Adb75613 Prostate
Adp45515 Human col
Aaw60983 Streptoco
Adh87756 Enterococ
Aab56508 Human pro
Ade54341 Rat Prote
Ade54337 Rat Prote
Ade54349 Rat Prote
Ade54345 Rat Prote
Aab87741 Human T2R
Aam40252 Human pol
Ade61720 Rat Prote
Ade61722 Human Pro
Adk67697 Human Rab
Aam42038 Human pol
Abg19562 Novel hum
Abu45936 Protein e
Adk48740 Streptoco
Adr95625 Novel S.
Adc96565 E. faeciu
Adj50364 Oil-assoc
Ado61905 Transcrip
Adn21114 Bacteri
Aab32256 HLA A0201
Aau68938 Human TAD
Adh13255 Human HLA
Adh78475 Human TAD
Aar21620 Sequence
Abg78461 Asparagin
Aar24891 Sequence
Adn197804 Sweet pot
Adn37732 Sweet pot
Adg59276 OGT relat
Aaw85067 Signal pe
Abb77593 Human can
Adn37752 Sweet pot
Aar55847 Human GCP
Aab49188 Lowest en
Aar55846 Human GCP
Aab30617 Streptoco
Abc59000 Human gen
Aar55845 Human GCP
Aar55849 Human GCP
Abb84647 Sweet pot
Adn37747 Sporamin
Aar74137 Potato sp

99	6	4.5	40	4	ABG54878	Abg54878 Human liv	172	6	4.5	98	4	AAU68923	Aau68923 Human SRC
100	6	4.5	41	5	ABG43008	Abg43008 Human pep	173	6	4.5	98	7	ADE13243	Ade13243 Scavenger
101	6	4.5	40	8	ADN37754	Adn37754 Sweet pot	174	6	4.5	98	8	ADH78452	Adh78452 Human TAD
102	6	4.5	42	2	AAI14007	Aay14007 Dnrk repe	175	6	4.5	99	4	AAO07330	Aao07330 Human pol
103	6	4.5	42	7	ADR83840	Abr83840 Escherich	176	6	4.5	100	2	AAI34819	Aay34819 Amino aci
104	6	4.5	42	6	ADF69983	Adf69983 AcMA-type	177	6	4.5	100	4	AAO00134	Aao00134 Human pol
105	6	4.5	42	7	ADP69979	Adf69979 AcMA-type	178	6	4.5	101	3	AAG54719	Aag54719 Arabidops
106	6	4.5	44	3	AB16864	Ab16864 Bacteriop	179	6	4.5	101	3	AAG54855	Aae24855 Human DED
107	6	4.5	45	4	ABE58480	Abb58480 Drosophil	180	6	4.5	101	5	AAE38898	Aae38898 Human DED
108	6	4.5	45	6	ABO14013	Abol14013 Novel hum	181	6	4.5	105	4	AAE07089	Aae07089 Human gen
109	6	4.5	45	8	ADN60710	Adn60710 Human sec	182	6	4.5	105	4	AAE07060	Aae07060 Human gen
110	6	4.5	46	2	AAI27608	Aay27608 Human sec	183	6	4.5	105	4	ABG65075	Abg65075 Human alb
111	6	4.5	46	6	ABU07202	Abu07202 Maize SSI	184	6	4.5	105	5	ABG65074	Abg65074 Human alb
112	6	4.5	46	8	ADG78419	Adg78419 Human sec	185	6	4.5	105	7	ABO72127	AbO72127 Pseudomon
113	6	4.5	50	7	ADE80757	Ade80757 Microsate	186	6	4.5	105	8	ADL78342	Adl78342 Albumin f
114	6	4.5	52	4	AAU57922	Aau57922 Propionib	187	6	4.5	105	8	ADL78341	Adl78341 Albumin f
115	6	4.5	52	6	ABM54441	Abm54441 Propionib	188	6	4.5	107	6	ABP76286	Abp76286 Human GEN
116	6	4.5	54	4	ABG14793	Abg14793 Novel hum	189	6	4.5	108	4	AAG91184	Aag91184 C glutami
117	6	4.5	57	4	AAU46439	Aau46439 Propionib	190	6	4.5	110	6	ABR39780	Abr39780 R. glutin
118	6	4.5	57	6	ABM42958	Abm42958 Propionib	191	6	4.5	110	7	ADC96062	Adc96062 E. faeciu
119	6	4.5	59	3	AAG12300	Aag12300 Zea mays	192	6	4.5	110	8	ADR10082	Adr10082 Human pro
120	6	4.5	62	5	ABP39591	Abp39591 Staphyloc	193	6	4.5	111	3	AAG17518	Aag17518 Arabidops
121	6	4.5	62	8	ADS05582	AdS05582 Staphyloc	194	6	4.5	111	4	ABBI0692	Abbi0692 Human pan
122	6	4.5	63	4	ADM84352	Adm84352 Human imm	195	6	4.5	111	4	AAI92990	Aai92990 Human dig
123	6	4.5	64	7	ADC97533	Adc97533 E. faeciu	196	6	4.5	111	4	AAE07115	Aae07115 Human gen
124	6	4.5	67	3	ABE56427	AbE56427 Human pro	197	6	4.5	112	3	AAI84445	Aay84445 Amino aci
125	6	4.5	67	8	ADJ67567	Adj67567 Human ova	198	6	4.5	112	3	AAG12299	Aag12299 Zea mays
126	6	4.5	67	8	ABO57060	AbO57060 Human gen	199	6	4.5	112	3	AAG45000	Aag45000 Zea mays
127	6	4.5	68	5	ABP39931	Abp39931 Staphyloc	200	6	4.5	112	3	AAG18819	Aag18819 Zea mays
128	6	4.5	69	5	ABP11387	Abp11387 Human ORF	201	6	4.5	112	6	ABJ25997	Abj25997 Aspergill
129	6	4.5	69	7	ADH35531	Adh35531 Partial s	202	6	4.5	113	2	AAW36449	Aaw36449 Human che
130	6	4.5	73	4	AAO12563	Aao12563 Human pol	203	6	4.5	113	5	ABW78092	Abw78092 Amino aci
131	6	4.5	75	2	AAE55843	Aae55843 Human GCP	204	6	4.5	113	6	ABG73739	Abg73739 Human Cka
132	6	4.5	75	2	AAW96720	Aaw96720 Granulocy	205	6	4.5	114	2	AAW46286	Aaw46286 Human gra
133	6	4.5	75	6	ABU67722	Abu67722 Human CX	206	6	4.5	114	5	AAU98084	Aau98084 Human SCY
134	6	4.5	75	7	ABO07356	AbO07356 Amino aci	207	6	4.5	114	6	ABU56721	Abu56721 Lung canc
135	6	4.5	75	7	ABE80889	Ade80889 GCP-2 che	208	6	4.5	114	6	ABJ25397	Abj25397 Aspergill
136	6	4.5	76	8	ADJ67568	Adj67568 Human ova	209	6	4.5	114	7	ABR44247	Abr44247 Human wil
137	6	4.5	77	3	AAI69024	Aay69024 Amino aci	210	6	4.5	114	7	ADE08120	Ade08120 Novel pro
138	6	4.5	77	3	AAO00878	Aao00878 Human sec	211	6	4.5	114	7	ADF90874	Adf90874 Human hep
139	6	4.5	77	5	AAO20029	Aao20029 Human che	212	6	4.5	114	7	ADN399146	Adn39146 Cancer/an
140	6	4.5	77	5	AAO14162	Aao14162 Human GCP	213	6	4.5	114	7	ADN39996	Adn39996 Cancer/an
141	6	4.5	77	8	ADH32782	Adh32782 Yeast smo	214	6	4.5	114	8	ADQ76206	Adq76206 Chemokine
142	6	4.5	77	8	ADR90680	Adr90680 Human gra	215	6	4.5	115	3	AAO00876	Aao00876 Human sec
143	6	4.5	79	4	ABG12182	Abg12182 Novel hum	216	6	4.5	115	7	ABR44248	Abr44248 Human gra
144	6	4.5	80	4	AAI19769	Aai19769 Peptide #	217	6	4.5	115	7	ADF07301	Adf07301 Bacterial
145	6	4.5	80	4	ABB39569	Abb39569 Peptide #	218	6	4.5	115	7	ADH86054	Adh86054 Enterococ
146	6	4.5	80	4	AAI33128	Aai33128 Peptide #	219	6	4.5	117	3	AAG46694	Aag46694 Arabidops
147	6	4.5	80	4	AAI81490	Aai81490 Human hae	220	6	4.5	117	4	ABB67424	Abb67424 Drosophil
148	6	4.5	80	4	ABB24287	Abb24287 Protein #	221	6	4.5	117	5	ABP06380	Abp06380 Human ORF
149	6	4.5	80	4	AAW72897	Aaw72897 Human bon	222	6	4.5	118	3	AAI5934	Aag15934 Arabidops
150	6	4.5	80	4	AAW60268	Aaw60268 Human bra	223	6	4.5	118	4	ABG09835	Abg09835 Novel hum
151	6	4.5	80	4	ABG54605	Abg54605 Human liv	224	6	4.5	118	7	ADM05266	Adm05266 Human pro
152	6	4.5	80	5	ABG42731	Abg42731 Human pep	225	6	4.5	119	7	ADF59699	Adf59699 Human pol
153	6	4.5	81	3	AAG44083	Aag44083 Arabidops	226	6	4.5	120	7	ADE87014	Ade87014 Human pan
154	6	4.5	82	8	ADK47218	Adk47218 Streptoco	227	6	4.5	121	5	ABP09077	Abp09077 Human ORF
155	6	4.5	83	5	ABP00060	Abp00060 Human ORF	228	6	4.5	122	4	AAI5773	Aai5773 Human rep
156	6	4.5	83	7	ADF08024	Adf08024 Bacterial	229	6	4.5	122	4	ABB96304	Abb96304 Human tes
157	6	4.5	84	4	AAU86706	Aau86706 Novel hum	230	6	4.5	122	4	ABG60289	Abg60289 Human ova
158	6	4.5	84	4	ABM63828	Abm63828 Propionib	231	6	4.5	122	5	ABG61760	Abg61760 Novel ova
159	6	4.5	84	6	ABM60347	Abm60347 Propionib	232	6	4.5	124	3	AAG58722	Aag58722 Arabidops
160	6	4.5	84	7	ADB60040	Abd60040 Connectiv	233	6	4.5	124	4	AAU22406	Aau22406 Human car
161	6	4.5	85	5	ADH32539	Adh32539 Yeast smo	234	6	4.5	124	4	AAW42367	Aaw42367 Human pol
162	6	4.5	86	4	ABB53005	Abb53005 Escherich	235	6	4.5	124	7	ADE46374	Ade46374 Human car
163	6	4.5	87	4	AAU61829	Aau61829 Propionib	236	6	4.5	124	8	ADJ07792	Adj07792 Human car
164	6	4.5	87	6	ABM58348	Abm58348 Propionib	237	6	4.5	125	5	ABP38617	Abp38617 Staphyloc
165	6	4.5	88	4	AAU14721	Aau14721 Novel bon	238	6	4.5	125	5	ABP51337	Abp51337 Human MDD
166	6	4.5	88	8	ADR40109	Adr40109 Human PKH	239	6	4.5	125	8	ADS05116	AdS05116 Staphyloc
167	6	4.5	90	4	AAO09955	Aao09955 Human pol	240	6	4.5	128	6	ABJ18793	Abj18793 Pseudomon
168	6	4.5	91	4	ABB16571	Abb16571 Human ner	241	6	4.5	129	5	Aau97865	Aau97865 Protein 1
169	6	4.5	92	2	AAI41535	Aai41535 M.ferment	242	6	4.5	133	3	AAG44082	Aag44082 Arabidops
170	6	4.5	93	5	ABG98438	Abg98438 Thermus t	243	6	4.5	133	5	ABP41276	Abp41276 Human ova
171	6	4.5	93	5	ABG73103	Abg73103 Human amy	244	6	4.5	133	5	ABP63803	Abp63803 Human ORF

245	6	4.5	133	8	ADR09540	Adr09540 Human pro	318	6	4.5	184	2	AAW90338	Aaw90338 Human DPl
246	6	4.5	134	8	ADG22447	Adg22447 Cyanophag	319	6	4.5	184	3	AAI12151	Aai12151 Hydrophob
247	6	4.5	135	5	ABP34525	Abp34525 Human ORF	320	6	4.5	184	3	AAO70200	Aao70200 Arabidops
248	6	4.5	136	2	AAW8980	Aaw8980 Polypepti	321	6	4.5	184	3	AAQ48968	Aaq48968 Arabidops
249	6	4.5	136	4	ABBS1056	Abbs1056 Human sec	322	6	4.5	184	3	AAQ07573	Aaq07573 Arabidops
250	6	4.5	136	6	ABO45313	Abos45313 Novel hum	323	6	4.5	184	4	AAW38817	Aaw38817 Human pol
251	6	4.5	137	7	ABO26793	Abos26793 Protein a	324	6	4.5	184	6	ABP70683	Abp70683 Rice acet
252	6	4.5	137	4	AAU53018	Aau53018 Propionib	325	6	4.5	184	7	ADIC37437	Adic37437 Nuclear f
253	6	4.5	137	6	ABM69897	Abm69897 Phototrab	326	6	4.5	185	7	ADI63093	Adi63093 Human apo
254	6	4.5	137	6	ABM49537	Abm49537 Propionib	327	6	4.5	185	3	AAQ54086	Aaq54086 Arabidops
255	6	4.5	138	3	AAQ21079	Aaq21079 Arabidops	328	6	4.5	186	4	ABG02352	Abg02352 Novel hum
256	6	4.5	139	7	AAO70116	Aao70116 Pseudomon	329	6	4.5	186	7	ADC32800	Adc32800 Human nov
257	6	4.5	140	8	ADR99471	Adr99471 Chlamydia	330	6	4.5	188	7	ADC32822	Adc32822 Human nov
258	6	4.5	141	8	ADR99443	Adr99443 Chlamydia	331	6	4.5	189	3	AAQ49061	Aaq49061 Arabidops
259	6	4.5	142	4	ABB11242	Abb11242 Human SLI	332	6	4.5	189	3	AAQ11287	Aaq11287 Arabidops
260	6	4.5	142	4	AAO05847	Aao05847 Human pol	333	6	4.5	190	6	AAO16327	Aao16327 Human pol
261	6	4.5	142	7	ADP08329	Adp08329 Novel pro	334	6	4.5	191	4	ABB67425	Abb67425 Drosophil
262	6	4.5	142	7	ADP60617	Adp60617 Human con	335	6	4.5	191	4	ABG12181	Abg12181 Novel hum
263	6	4.5	142	8	ADR99387	Adr99387 Chlamydia	336	6	4.5	192	8	ABOS8647	Abos8647 Human gen
264	6	4.5	144	3	AAQ55068	Aaq55068 Arabidops	337	6	4.5	193	2	AAW23619	Aaw23619 Prolactin
265	6	4.5	145	3	AAQ04272	Aaq04272 Arabidops	338	6	4.5	197	3	AAQ23591	Aaq23591 Arabidops
266	6	4.5	145	6	ADA34914	Ada34914 Acinetoba	339	6	4.5	197	6	ABU09847	Abu09847 Rat prola
267	6	4.5	147	3	AAQ44999	Aaq44999 Zea mays	340	6	4.5	197	6	ADB08530	Adb08530 Alloiococ
268	6	4.5	147	6	ADB08528	Adb08528 Alloiococ	341	6	4.5	198	2	AAQ22494	Aaq22494 Rat prola
269	6	4.5	150	3	AAQ21078	Aaq21078 Arabidops	342	6	4.5	198	6	ADA48256	Ada48256 Rice prot
270	6	4.5	151	2	AAQ37664	Aaq37664 Protein w	343	6	4.5	198	6	ADA48574	Ada48574 Rice prot
271	6	4.5	152	2	AAQ35292	Aaq35292 Chlamydia	344	6	4.5	199	4	AAO00877	Aao00877 Human bon
272	6	4.5	154	4	ABG12922	Abg12922 Novel hum	345	6	4.5	199	5	ABP41275	Abp41275 Human ova
273	6	4.5	154	7	ADP04497	Adp04497 Bacterial	346	6	4.5	200	4	AAO40603	Aao40603 Human pol
274	6	4.5	155	3	AAQ15933	Aaq15933 Arabidops	347	6	4.5	200	7	ADH85998	Adh85998 Enterococ
275	6	4.5	156	2	AAQ25008	Aaq25008 Yeast YAP	348	6	4.5	202	2	AAQ39323	Aaq39323 S. spinos
276	6	4.5	156	3	AAQ54087	Aaq54087 Arabidops	349	6	4.5	202	4	AAO00896	Aao00896 Human bon
277	6	4.5	156	3	AAQ11288	Aaq11288 Arabidops	350	6	4.5	202	6	ABU18571	Abu18571 Protein e
278	6	4.5	156	6	ABR53857	Abpr53857 Protein s	351	6	4.5	202	6	ABU20918	Abu20918 Protein e
279	6	4.5	156	7	ADK64922	Adk64922 Disease t	352	6	4.5	202	6	ABU20869	Abu20869 Protein e
280	6	4.5	157	2	AAQ08307	Aaq08307 Human CBC	353	6	4.5	205	4	ABU86168	Abu86168 A. thalia
281	6	4.5	157	3	AAQ04271	Aaq04271 Arabidops	354	6	4.5	205	4	AAO06682	Aao06682 Human pol
282	6	4.5	157	4	AAU23312	Aau23312 Novel hum	355	6	4.5	206	7	ADC35090	Adc35090 Human bre
283	6	4.5	157	8	ADP24096	Adp24096 PRO polyp	356	6	4.5	207	4	ABG30286	Abg30286 Novel hum
284	6	4.5	158	8	ADK99291	Adk99291 Streptoco	357	6	4.5	207	4	ABG18189	Abg18189 Novel hum
285	6	4.5	159	4	ADK09853	Adk09853 Novel hum	358	6	4.5	207	5	ABP43634	Abp43634 FLJ20509
286	6	4.5	159	8	ADK16691	Adk16691 Nanoarcha	359	6	4.5	208	3	AAQ97386	Aaq97386 Arabidops
287	6	4.5	160	2	AAQ37059	Aaq37059 Protein i	360	6	4.5	208	4	AAO04153	Aao04153 Arabidops
288	6	4.5	160	6	ADA48584	Ada48584 Rice prot	361	6	4.5	208	5	AAE20526	Aae20526 Arabidops
289	6	4.5	160	6	ADA47984	Ada47984 Rice prot	362	6	4.5	208	5	AAE21532	Aae21532 Arabidops
290	6	4.5	161	4	ABG09854	Abg09854 Novel hum	363	6	4.5	208	5	ABP79064	Abp79064 Mature ar
291	6	4.5	164	3	AAQ21077	Aaq21077 Arabidops	364	6	4.5	208	6	ABU11293	Abu11293 Arabidops
292	6	4.5	164	8	ADK99292	Adk99292 Streptoco	365	6	4.5	211	4	AAQ81246	Aaq81246 Human AFP
293	6	4.5	165	7	ADC94956	Adc94956 E. faeciu	366	6	4.5	212	4	ADMI19920	Admi19920 Protein e
294	6	4.5	165	7	ADC94955	Adc94955 E. faeciu	367	6	4.5	213	4	AAAB86945	Aaab86945 Human 60S
295	6	4.5	166	6	ADA33772	Ada33772 Acinetoba	368	6	4.5	214	4	AAAB86941	Aaab86941 Human chr
296	6	4.5	168	4	AAO02532	Aao02532 Human pol	369	6	4.5	214	4	AAAB86942	Aaab86942 Human chr
297	6	4.5	171	3	AAQ04270	Aaq04270 Arabidops	370	6	4.5	214	6	AAO19616	Aao19616 Human nuc
298	6	4.5	173	3	AAQ15932	Aaq15932 Arabidops	371	6	4.5	214	6	ABU24035	Abu24035 Protein e
299	6	4.5	177	4	AAU17268	Aau17268 Novel sig	372	6	4.5	214	7	ADB82785	Adb82785 Human pro
300	6	4.5	177	4	ABO30377	Abos30377 Human exp	373	6	4.5	214	8	ABM82464	Abm82464 Tumour-as
301	6	4.5	177	4	AAW96370	Aaw96370 Human rep	374	6	4.5	214	8	ADP25310	Adp25310 PRO polyp
302	6	4.5	177	4	ABB10934	Abb10934 Human ova	375	6	4.5	215	6	ABP77878	Abp77878 N. gonorr
303	6	4.5	177	4	AAU87414	Aau87414 Novel cen	376	6	4.5	216	1	AAQ61024	Aaq61024 Plasmid p
304	6	4.5	177	4	AAU87688	Aau87688 Novel cen	377	6	4.5	216	2	AAQ11839	Aaq11839 Sporamin
305	6	4.5	177	7	ADB93976	Adb93976 Human nov	378	6	4.5	217	4	AAE04102	Aae04102 Human gen
306	6	4.5	177	8	ADI54729	Adi54729 Novel hum	379	6	4.5	217	4	AAAM41591	Aaam41591 Human pol
307	6	4.5	177	8	ADI55003	Adi55003 Novel hum	380	6	4.5	217	5	ABG64382	Abg64382 Human alb
308	6	4.5	180	2	AAQ35323	Aaq35323 Chlamydia	381	6	4.5	217	6	ADA41058	Ada41058 Human sec
309	6	4.5	180	4	AAE04177	Aae04177 Human gen	382	6	4.5	217	7	ADC74303	Adc74303 Human sec
310	6	4.5	180	6	ABU26771	Abu26771 Protein e	383	6	4.5	217	8	ADL77649	Adl77649 Albumin f
311	6	4.5	181	3	AAAB1713	Aaab1713 Human ORF	384	6	4.5	218	8	ADN17666	Adn17666 Bacterial
312	6	4.5	182	2	AAQ48296	Aaq48296 Human PGF	385	6	4.5	218	2	AAW99177	Aaw99177 RasGAP ca
313	6	4.5	182	4	AAU29433	Aau29433 Human G p	386	6	4.5	218	2	AAW99162	Aaw99162 RasGAP ca
314	6	4.5	182	5	ABG60721	Abg60721 Novel G p	387	6	4.5	218	4	AAE06613	Aae06613 Human pro
315	6	4.5	183	3	AAQ34111	Aaq34111 Zea mays	388	6	4.5	218	4	ABE66330	Abbe66330 Drosophil
316	6	4.5	183	5	ABP26401	Abp26401 Streptoco	389	6	4.5	218	5	ABR40479	Abra40479 Human sec
317	6	4.5	183	8	ADK99290	Adk99290 Streptoco	390	6	4.5	218	6	ABB82956	Abb82956 Human PRO

391	6	4.5	218	7	ADG75738	Human pro	464	6	4.5	240	3	AAG34109	Zea mays
392	6	4.5	219	1	AP61023	Plasmid p	465	6	4.5	240	3	AAG48966	Arabidops
393	6	4.5	219	2	AAR11802	Sporamin	466	6	4.5	240	3	AAG25606	Arabidops
394	6	4.5	219	4	AAE10856	Sweet pot	467	6	4.5	240	3	AAG07571	Arabidops
395	6	4.5	219	4	AAE04128	Human gen	468	6	4.5	240	5	ABB07959	Rat LR (r
396	6	4.5	219	4	AAE04127	Human gen	469	6	4.5	241	3	AAG49060	Arabidops
397	6	4.5	219	5	ASG64381	Human alb	470	6	4.5	241	4	ABG11558	Novel hum
398	6	4.5	219	5	ASG64380	Human alb	471	6	4.5	242	2	AAAY1194	S. pneumo
399	6	4.5	219	6	ADA41417	Human sec	472	6	4.5	242	3	AAAY81732	Streptoco
400	6	4.5	219	6	ADA41418	Human sec	473	6	4.5	242	6	ABU02727	S. pneumo
401	6	4.5	219	7	ADC74551	Human sec	474	6	4.5	242	8	ADK47839	Streptoco
402	6	4.5	219	7	ADC74550	Human sec	475	6	4.5	243	5	ABP42317	Human ova
403	6	4.5	219	8	ADL77648	Albumin f	476	6	4.5	244	8	ADN17928	Bacterial
404	6	4.5	219	8	ADL77647	Albumin f	477	6	4.5	245	4	ABB65836	Drosophil
405	6	4.5	220	2	AAR60770	Maize QM	478	6	4.5	245	7	ADB65312	Human pro
406	6	4.5	220	2	AAAY05721	Gluconate	479	6	4.5	246	5	ABP38330	Staphyloc
407	6	4.5	220	3	AAG34110	Zea mays	480	6	4.5	246	8	ADS04851	Staphyloc
408	6	4.5	220	6	ABR52601	Protein s	481	6	4.5	247	6	ABM71082	Staphyloc
409	6	4.5	220	7	ADK63900	Disease t	482	6	4.5	248	3	AAG25605	Arabidops
410	6	4.5	220	8	ADS42682	Bacterial	483	6	4.5	248	4	ABB60027	Drosophil
411	6	4.5	221	3	AAG34633	Arabidops	484	6	4.5	249	3	AAB28001	Human sec
412	6	4.5	221	3	AAG07199	Arabidops	485	6	4.5	249	3	AAB28002	Human sec
413	6	4.5	221	3	AAG48967	Arabidops	486	6	4.5	252	4	AAG71966	Human olf
414	6	4.5	221	3	AAG07572	Arabidops	487	6	4.5	252	5	ABG60232	Human G p
415	6	4.5	221	6	ADA26318	Oncoprote	488	6	4.5	252	7	ADB70009	C. neofor
416	6	4.5	221	7	ABU62142	C-Jun N-t	489	6	4.5	254	7	ADC85615	Human GPC
417	6	4.5	221	7	ADJ64025	B-Jun N-t	490	6	4.5	257	8	ABU25091	Novel S.
418	6	4.5	222	3	AAAB16712	Bacterioph	491	6	4.5	258	6	ABU25091	Protein e
419	6	4.5	223	7	ADJ21645	Novel hum	492	6	4.5	260	2	AAAY34541	Porphorym
420	6	4.5	223	7	ABO71431	Pseudomon	493	6	4.5	260	7	ADM47235	NK recept
421	6	4.5	223	8	ABO58832	Human gen	494	6	4.5	261	6	ABU21604	Protein e
422	6	4.5	224	3	AAG33417	Zea mays	495	6	4.5	262	4	AAU23380	Novel hum
423	6	4.5	224	7	ADE08523	Novel pro	496	6	4.5	262	4	AAU21782	Novel hum
424	6	4.5	225	1	AAAP82078	Recombina	497	6	4.5	262	7	ADC46423	Human neo
425	6	4.5	225	4	AAU18692	Renal and	498	6	4.5	264	2	AAR56499	TATA-bind
426	6	4.5	225	4	AAU20567	Human nov	499	6	4.5	264	2	AAW06089	Human TAT
427	6	4.5	225	5	ABR16986	Human rib	500	6	4.5	264	2	AAW25016	TATA-bind
428	6	4.5	225	5	ABR78570	Human rib	501	6	4.5	265	6	ABU11742	Human MDD
429	6	4.5	226	2	AAAR14599	Rat prola	502	6	4.5	266	2	AAAY34407	Porphorym
430	6	4.5	226	2	AAAR14599	Rat prola	503	6	4.5	267	4	AAAM80238	Human pro
431	6	4.5	226	4	ABG12160	Novel hum	504	6	4.5	268	8	ADR66894	Human pro
432	6	4.5	226	6	ABU23549	Protein e	505	6	4.5	268	8	ADR65996	Human pro
433	6	4.5	229	4	AAG98977	E. coli g	506	6	4.5	270	3	AAG12989	Arabidops
434	6	4.5	229	6	ABR41691	Human DIT	507	6	4.5	270	3	AAG05237	Arabidops
435	6	4.5	229	8	ADK99196	Streptoco	508	6	4.5	270	3	AAG50049	Arabidops
436	6	4.5	229	8	ADK99197	Streptoco	509	6	4.5	271	3	AAAY97392	Arabidops
437	6	4.5	230	8	ADK99195	Streptoco	510	6	4.5	271	3	AAG50048	Arabidops
438	6	4.5	230	8	ADK99194	Streptoco	511	6	4.5	271	3	AAG05236	Arabidops
439	6	4.5	232	6	ABU24519	Protein e	512	6	4.5	271	4	ABU04159	Arabidops
440	6	4.5	232	6	ABU23640	Protein e	513	6	4.5	271	5	AAE20532	Arabidops
441	6	4.5	233	3	AAAY59412	Human CIP	514	6	4.5	271	5	AAE21538	Arabidops
442	6	4.5	233	4	ABG10183	Novel hum	515	6	4.5	271	5	AAE18646	Human G-p
443	6	4.5	233	7	ABM85809	Human hea	516	6	4.5	271	5	ABB79070	Arabidops
444	6	4.5	233	7	ABM85808	Human pro	517	6	4.5	271	5	ABP65955	Bifidobac
445	6	4.5	233	8	ADO15479	Human Bcl	518	6	4.5	271	6	ABU11299	Arabidops
446	6	4.5	233	8	ADR87467	Rat B-cel	519	6	4.5	275	3	AAG34632	Arabidops
447	6	4.5	233	8	ADR87463	Human B-c	520	6	4.5	275	8	ADN46744	Thermococ
448	6	4.5	234	5	ABR40410	Human sec	521	6	4.5	276	5	ABP43635	FLJ20509
449	6	4.5	234	5	ADJ28009	ECMCAL pr	522	6	4.5	277	4	AAAM39805	Human pol
450	6	4.5	234	6	ABR43632	Mouse CLA	523	6	4.5	279	6	ABU19100	Protein e
451	6	4.5	234	6	ADB11894	Alliococ	524	6	4.5	281	5	ABJ04730	GPCR 10 p
452	6	4.5	234	7	ADC95656	E. faeciu	525	6	4.5	284	3	AAG16499	Arabidops
453	6	4.5	234	7	ADI21249	Novel hum	526	6	4.5	284	3	AAG39487	Arabidops
454	6	4.5	234	8	ADK60179	Angiogene	527	6	4.5	284	4	AAE10804	A. thalia
455	6	4.5	234	8	ADK60480	Angiogene	528	6	4.5	284	6	ABU34729	Protein e
456	6	4.5	234	8	ADP73103	Angiogene	529	6	4.5	284	6	ABU35121	Protein e
457	6	4.5	235	3	AAG07198	Arabidops	530	6	4.5	284	6	ADA89376	A. thalia
458	6	4.5	235	4	ABG17696	Novel hum	531	6	4.5	285	2	AAW72751	Streptoco
459	6	4.5	235	4	ABG18326	Novel hum	532	6	4.5	286	4	AAB86946	Human ak0
460	6	4.5	236	4	AAE04178	Human gen	533	6	4.5	286	4	AAAB79376	Corynebac
461	6	4.5	237	2	AAW38641	S. pneumo	534	6	4.5	287	5	AAO18609	Synechocy
462	6	4.5	238	3	AAG21622	Arabidops	535	6	4.5	287	8	ADS42462	Bacterial
463	6	4.5	238	5	ABB92058	Herbicida	536	6	4.5	289	2	AAAY85811	S. pneumo

537	6	4.5	290	5	ABB72326	Abb72326 Rat prote	610	322	7	ADB80350	Adb80350 Human MDD
538	6	4.5	290	7	ADM47237	Adm47237 NK recept	611	323	7	ADM03762	Adm03762 Human pro
539	6	4.5	294	3	AAE32247	AAe32247 Tumour as	612	324	3	AAy75254	AAy75254 Neisseria
540	6	4.5	294	4	AAU68912	AAu68912 Human TAG	613	324	3	AAy75253	AAy75253 Neisseria
541	6	4.5	294	5	AAU78125	AAu78125 Human vom	614	324	3	AAy75255	AAy75255 Neisseria
542	6	4.5	294	6	AAE37057	AAe37057 Human gen	615	324	6	ABP77231	ABp77231 N. gonorr
543	6	4.5	294	6	AAE37072	AAe37072 Human gen	616	325	7	ABO71675	ABo71675 Pseudomon
544	6	4.5	294	6	ABR40104	ABr40104 Human cel	617	326	4	RAB60387	Rab60387 Human apo
545	6	4.5	294	7	ADE08376	Ade08376 Novel pro	618	326	5	ABB07263	ABb07263 Human apo
546	6	4.5	294	7	ADE13230	Ade13230 Human spl	619	326	7	ADC95799	Adc95799 E. faeciu
547	6	4.5	294	7	ADP05633	Adp05633 Bacterial	620	326	7	ADC73260	Adc73260 Human DED
548	6	4.5	294	7	ADM47211	Adm47211 Pheromone	621	327	2	AAR97845	Aar97845 Kaposi's
549	6	4.5	294	7	ADN95111	Adn95111 Human LEC	622	327	2	AAR93617	Aar93617 Kaposi's
550	6	4.5	295	8	ADH78439	Adh78439 Human tum	623	327	5	RAY72093	Ray72093 Human ser
551	6	4.5	295	3	AGS29139	AGs29139 Arabidops	624	327	5	ABG30790	ABg30790 Human ser
552	6	4.5	295	6	ABU48615	ABu48615 Protein e	625	327	5	AAE17921	AAe17921 Human gen
553	6	4.5	295	8	ADL04933	ADl04933 M. catarr	626	327	8	ADQ26095	Adq26095 Transmemb
554	6	4.5	296	8	ABO58743	ABo58743 Human gen	627	327	8	ADQ26096	Adq26096 Transmemb
555	6	4.5	297	3	AGS29138	AGs29138 Arabidops	628	329	4	RAM89960	RAm89960 Human imm
556	6	4.5	297	8	ADS28869	ADs28869 Bacterial	629	332	6	ABU01726	ABu01726 S. pneumo
557	6	4.5	298	6	ABR82559	ABr82559 Human chr	630	332	8	ADM92177	ADm92177 S. pneumo
558	6	4.5	298	7	ADD30540	AdD30540 Plant vie	631	335	6	ABU27128	ABu27128 Protein e
559	6	4.5	298	8	ADI44015	ADi44015 Plant tra	632	336	6	ABR42499	ABr42499 Coumerync
560	6	4.5	300	2	AAV16108	AAv16108 A formate	633	336	6	ABR42540	ABr42540 Clorobloc
561	6	4.5	300	7	ADH87377	ADh87377 Enterococ	634	336	7	ADJ94942	ADj94942 Novel NOV
562	6	4.5	303	4	ABE60386	ABe60386 Human apo	635	336	7	ADJ94962	ADj94962 Novel NOV
563	6	4.5	304	3	ABE15551	ABe15551 Apoptosis	636	336	8	ADO42203	ADo42203 Human NOV
564	6	4.5	304	3	AGS33416	AGs33416 Zea maye	637	336	8	ADO42207	ADo42207 Human NOV
565	6	4.5	305	8	ABM84152	ABm84152 Human dia	638	336	8	ADQ67568	ADq67568 Novel hum
566	6	4.5	305	8	ADN19514	ADn19514 Bacterial	639	337	8	ADS10930	ADs10930 Human the
567	6	4.5	305	8	ADN17509	ADn17509 Bacterial	640	337	8	ADR10320	ADr10320 Human pro
568	6	4.5	307	2	AAE84567	AAe84567 Trypanoso	641	338	3	AGL16972	AGl16972 Arabidops
569	6	4.5	307	4	AG74832	AG74832 Human col	642	338	6	ABP72962	ABp72962 Amino aci
570	6	4.5	307	4	AAU39710	AAu39710 Propionib	643	340	3	AGS33415	AGs33415 Zea maye
571	6	4.5	307	4	AGS90155	AGs90155 C. Glutami	644	342	7	ADF76645	ADf76645 Novel hum
572	6	4.5	307	6	ABM36229	ABm36229 Propionib	645	342	8	ADJ66527	ADj66527 WD-repeat
573	6	4.5	308	2	AAW52194	AAw52194 Human gly	646	342	8	ADS88398	ADs88398 Human pro
574	6	4.5	308	3	AGS39486	AGs39486 Arabidops	647	342	8	ADN25409	ADn25409 Bacterial
575	6	4.5	308	4	ABE92940	ABe92940 Human pro	648	344	7	ADD26726	ADd26726 Human adi
576	6	4.5	308	5	ABP27280	ABp27280 Streptoco	649	344	7	ADE13369	ADe13369 Human spl
577	6	4.5	308	5	ABP56625	ABp56625 Human ste	650	344	8	ADL91867	ADl91867 Human PRO
578	6	4.5	308	8	ADK99193	ADk99193 Streptoco	651	344	8	ADQ26097	ADq26097 Transmemb
579	6	4.5	308	8	ADS88208	ADs88208 Human pro	652	346	5	AAU74748	AAu74748 Human pro
580	6	4.5	309	3	AGL16498	AGl16498 Arabidops	653	346	8	ADS24068	ADs24068 Bacterial
581	6	4.5	309	4	AG72262	AG72262 Human olf	654	348	3	AGG44528	AGg44528 Arabidops
582	6	4.5	309	4	AAU24707	AAu24707 Human olf	655	348	3	AGS54097	AGs54097 Arabidops
583	6	4.5	309	5	ABP95840	ABp95840 Human GPC	656	348	3	AGS54144	AGs54144 Arabidops
584	6	4.5	309	5	AAU85327	AAu85327 G-coupled	657	349	3	AGG43785	AGg43785 Arabidops
585	6	4.5	309	6	ABU11156	ABu11156 Human G-p	658	349	7	ADM25918	ADm25918 Hyperther
586	6	4.5	309	7	ADC85743	ADc85743 Human GPC	659	350	3	AGG43784	AGg43784 Arabidops
587	6	4.5	312	3	AGS25604	AGs25604 Arabidops	660	351	3	AGG54096	AGg54096 Arabidops
588	6	4.5	312	5	AAU95772	AAu95772 Human olf	661	351	3	AGG44527	AGg44527 Arabidops
589	6	4.5	312	6	ABU11162	ABu11162 Human G-p	662	351	3	AGS54143	AGs54143 Arabidops
590	6	4.5	312	6	AAO16329	AAo16329 Human pol	663	352	7	ADM47229	ADm47229 NK recept
591	6	4.5	312	7	ADC85967	ADc85967 Human GPC	664	352	7	ADM47227	ADm47227 NK recept
592	6	4.5	312	8	ADG83516	ADg83516 Human Olf	665	353	8	ADN18771	ADn18771 Bacterial
593	6	4.5	313	5	AAO17809	AAo17809 H influen	666	354	7	ABM85235	ABm85235 Human pro
594	6	4.5	314	6	AAO16330	AAo16330 Human pol	667	354	8	ADN21071	ADn21071 Bacterial
595	6	4.5	316	5	ABP41228	ABp41228 Human ova	668	355	2	AAW72750	AAw72750 Streptoco
596	6	4.5	317	5	ADE36453	ADe36453 Human PAN	669	355	5	ABP26355	ABp26355 Streptoco
597	6	4.5	317	7	ADM80187	ADm80187 Human NOV	670	355	6	ABU01818	ABu01818 S. pneumo
598	6	4.5	317	8	ADJ19375	ADj19375 Human PAN	671	355	7	ADH48628	ADh48628 3-dehydro
599	6	4.5	318	5	AAE24860	AAe24860 Human DED	672	355	7	ADH48630	ADh48630 Experimen
600	6	4.5	318	5	AAE38903	AAe38903 Human DED	673	355	8	ADK47027	ADk47027 Streptoco
601	6	4.5	318	6	ABU36529	ABu36529 Protein e	674	356	7	ADC96659	Adc96659 E. faeciu
602	6	4.5	318	6	ABR55201	ABr55201 Amino aci	675	356	3	RAY59147	Ray59147 E. niGula
603	6	4.5	319	3	ABE58420	ABe58420 Lung canc	676	360	8	ADJ70582	ADj70582 Human hea
604	6	4.5	320	5	ABG76848	ABg76848 Human G-p	677	360	8	ADS29093	ADs29093 Bacterial
605	6	4.5	321	3	AGS34631	AGs34631 Arabidops	678	361	5	ABB91364	ABb91364 Herbicida
606	6	4.5	321	5	ABE90173	ABe90173 Human PAN	679	361	5	ABB06038	ABb06038 Human NS
607	6	4.5	321	8	ADJ19416	ADj19416 Human PAN	680	361	8	ADR95298	ADr95298 Novel S.
608	6	4.5	322	6	ABM67907	ABm67907 Photorhab	681	364	2	AAW88979	AAw88979 Polypepti
609	6	4.5	322	7	ABM74226	ABm74226 DNA clone	682	364	4	ABB51055	ABb51055 Human sec

683	6	4.5	364	6	ABO45312	Novel hum	756	6	4.5	430	7	ADH87840	Enterococ
684	6	4.5	364	7	ABO26792	Protein a	757	6	4.5	434	2	ADI21173	Novel hum
685	6	4.5	365	7	ADM47231	NK recept	758	6	4.5	436	2	AAO35033	Chlamydia
686	6	4.5	366	4	AG73852	Humar. col	759	6	4.5	438	7	AAO30835	Human cel
687	6	4.5	366	8	ADN24099	Bacterial	760	6	4.5	438	8	ABO84996	Murine hum
688	6	4.5	367	7	ADE08721	Novel pro	761	6	4.5	439	4	ABG17899	Novel hum
689	6	4.5	368	4	AAB88516	Haemphil	762	6	4.5	439	7	ABM85234	Mouse pro
690	6	4.5	368	5	ABE06039	Human. NS	763	6	4.5	439	8	ADM05434	Atsipori
691	6	4.5	368	5	AAU91447	Haemphil	764	6	4.5	441	5	ABP30345	Streptoco
692	6	4.5	368	6	ABU49003	Protein e	765	6	4.5	442	4	ABO70328	Drosophil
693	6	4.5	368	6	ABU30152	Protein e	766	6	4.5	442	7	ABO65176	Klebsiell
694	6	4.5	370	7	ADC26994	Sorangium	767	6	4.5	443	6	AAO23300	Chimpanze
695	6	4.5	373	6	ABU29847	Protein e	768	6	4.5	443	6	AAO23297	Chimpanze
696	6	4.5	373	7	ABO75799	Pseudomon	769	6	4.5	444	4	ABG30309	Novel hum
697	6	4.5	374	4	AAU34978	Enterococ	770	6	4.5	444	8	ADA44475	Bacterial
698	6	4.5	374	6	ABU29288	Protein e	771	6	4.5	445	8	AAO23294	Chimpanze
699	6	4.5	374	8	ADS51929	TRMU SRQ	772	6	4.5	448	3	AAO21060	Herbicida
700	6	4.5	374	8	ADS51927	TRMU SRQ	773	6	4.5	448	5	ABG93980	Herbicida
701	6	4.5	375	4	ABB59643	Drosophil	774	6	4.5	448	8	ADO70390	Unidentif
702	6	4.5	376	5	ABP69074	Human pol	775	6	4.5	449	5	ABP28127	Streptoco
703	6	4.5	376	7	ADF06455	Bacterial	776	6	4.5	451	5	ABB47379	Listeria
704	6	4.5	377	6	ABP57041	Leucnosc	777	6	4.5	451	6	ABU44258	Human PRO
705	6	4.5	382	7	ADH85944	Enterococ	778	6	4.5	452	2	AAU41694	Human PRO
706	6	4.5	383	7	ADF07147	Bacterial	779	6	4.5	453	3	ABA44250	Human PRO
707	6	4.5	385	4	ABA896162	Putative	780	6	4.5	453	4	AAU29055	Human PRO
708	6	4.5	386	8	ADN25400	Bacterial	781	6	4.5	453	4	AAE06935	Human mem
709	6	4.5	387	4	AAB61911	R. anatip	782	6	4.5	453	5	AAO18402	Human ser
710	6	4.5	389	6	AAE32773	Mycobacte	783	6	4.5	453	5	ABJ05565	Breast ca
711	6	4.5	389	6	ABU27679	Protein e	784	6	4.5	453	5	AAE23020	Human tly
712	6	4.5	389	7	ADE47794	Human NOV	785	6	4.5	453	5	ABU58431	Human PRO
713	6	4.5	389	8	ADJ79064	Human NOV	786	6	4.5	453	6	ABU87979	Novel hum
714	6	4.5	390	3	AB442083	Human ORF	787	6	4.5	453	6	ABU84294	Human sec
715	6	4.5	391	6	ABU49026	Protein e	788	6	4.5	453	6	ABR66168	Human sec
716	6	4.5	392	6	ABU33486	Protein e	789	6	4.5	453	6	ABR65558	Human sec
717	6	4.5	393	6	ABU45467	Protein e	790	6	4.5	453	6	ABU99498	Human sec
718	6	4.5	394	5	ABP41994	Human ova	791	6	4.5	453	6	ABU82737	Human PRO
719	6	4.5	396	6	ABU49963	Protein e	792	6	4.5	453	6	ABU89858	Novel hum
720	6	4.5	396	7	ADM47225	NK recept	793	6	4.5	453	6	ABR58549	Human can
721	6	4.5	397	6	ABU31578	Protein e	794	6	4.5	453	6	ABR68107	Human sec
722	6	4.5	397	6	ABU48064	Protein e	795	6	4.5	453	6	ABU96160	Novel hum
723	6	4.5	397	6	ABU15199	Protein e	796	6	4.5	453	6	ABU92591	Human sec
724	6	4.5	397	6	ABU47088	Protein e	797	6	4.5	453	6	ABO08668	Human sec
725	6	4.5	397	8	ABM84413	Human dia	798	6	4.5	453	6	ABO02720	Human sec
726	6	4.5	398	4	ABE59789	Drosophil	799	6	4.5	453	6	ABR74874	Human sec
727	6	4.5	399	8	ABM84412	Human dia	800	6	4.5	453	6	ABR94636	Human sec
728	6	4.5	400	4	ABG13840	Novel hum	801	6	4.5	453	6	ABO25196	Novel hum
729	6	4.5	400	7	ABO61409	Klebsiell	802	6	4.5	453	6	ABU85609	Human PRO
730	6	4.5	401	7	ABO78452	Pseudomon	803	6	4.5	453	6	ABU98769	Novel hum
731	6	4.5	402	6	ABU37636	Protein e	804	6	4.5	453	6	ABU97984	Novel hum
732	6	4.5	404	7	ADI21301	Novel hum	805	6	4.5	453	6	ABU91690	Novel hum
733	6	4.5	405	7	ABM74083	DNA clone	806	6	4.5	453	6	ABU72202	Novel hum
734	6	4.5	405	7	ADM25877	Hyperther	807	6	4.5	453	6	ABU89383	Human PRO
735	6	4.5	407	6	ABM67888	Phototrab	808	6	4.5	453	6	ABU86224	Human sec
736	6	4.5	409	4	ABG21247	Novel hum	809	6	4.5	453	6	ABU67437	Human sec
737	6	4.5	411	4	AAE12586	Pseudomon	810	6	4.5	453	6	ABU80465	Human PRO
738	6	4.5	412	4	ABG21571	Novel hum	811	6	4.5	453	6	ABR99383	Human sec
739	6	4.5	419	6	ABU16307	Protein e	812	6	4.5	453	6	ABR98773	Human sec
740	6	4.5	419	8	ABM72236	Staphyloc	813	6	4.5	453	6	ABO16296	Human sec
741	6	4.5	419	8	ADH22284	ORF1 prot	814	6	4.5	453	6	ABR92196	Human sec
742	6	4.5	422	2	AAW56275	Flavobact	815	6	4.5	453	6	ABO18837	Human sec
743	6	4.5	424	6	ABU50519	Protein e	816	6	4.5	453	6	ABR78258	Human sec
744	6	4.5	424	6	ABU32398	Protein e	817	6	4.5	453	6	ABU56617	Lung canc
745	6	4.5	425	2	AAW98019	Mouse cal	818	6	4.5	453	6	ABO49994	Novel hum
746	6	4.5	425	5	ABE99106	Mouse int	819	6	4.5	453	6	ABO00133	Novel hum
747	6	4.5	425	6	ABP56662	Chimpanze	820	6	4.5	453	6	ABO11465	Human sec
748	6	4.5	426	4	AAU16773	Peptide #	821	6	4.5	453	6	ABO02110	Human sec
749	6	4.5	426	4	ABB30593	Peptide #	822	6	4.5	453	6	ABU88684	Novel hum
750	6	4.5	426	4	AAW56567	Human bra	823	6	4.5	453	6	ABU83379	Human sec
751	6	4.5	426	4	AAW04490	Peptide #	824	6	4.5	453	6	ABO06180	Novel hum
752	6	4.5	426	5	ABG38533	Human pep	825	6	4.5	453	6	ABR59216	Human sec
753	6	4.5	428	6	ABU25307	Protein e	826	6	4.5	453	6	ABO09278	Human sec
754	6	4.5	428	6	ABU29208	Protein e	827	6	4.5	453	6	ABO19142	Novel hum
755	6	4.5	428	7	ADM47233	NK recept	828	6	4.5	453	6	ABO11160	Human sec

829	6	4.5	453	6	ABR66778	Human sec	902	6	4.5	453	6	ABO09888	Human sec
830	6	4.5	453	6	ABO15991	Human sec	903	6	4.5	453	6	ABO08973	Human sec
831	6	4.5	453	6	ABO13697	Human sec	904	6	4.5	453	6	ABU10541	Human sec
832	6	4.5	453	6	ABU84882	Human sec	905	6	4.5	453	6	ABU95550	Human PRO
833	6	4.5	453	6	ABU65600	Human sec	906	6	4.5	453	6	ABU96759	Novel hum
834	6	4.5	453	6	ABO07448	Human PRO	907	6	4.5	453	6	ABR70604	Human sec
835	6	4.5	453	6	ABO03635	Human sec	908	6	4.5	453	6	ABO04955	Novel hum
836	6	4.5	453	6	ABR67083	Human sec	909	6	4.5	453	6	ABO08363	Human sec
837	6	4.5	453	6	ABU15686	Human sec	910	6	4.5	453	6	ABO05570	Human sec
838	6	4.5	453	6	ABU55967	Human sec	911	6	4.5	453	6	ABR73959	Human sec
839	6	4.5	453	6	ABU61080	Human PRO	912	6	4.5	453	6	ABR95551	Human sec
840	6	4.5	453	6	ABU65295	Human PRO	913	6	4.5	453	6	ABR80848	Human sec
841	6	4.5	453	6	ABU95240	Novel hum	914	6	4.5	453	6	ABR81153	Human sec
842	6	4.5	453	6	ABU71143	Human PRO	915	6	4.5	453	6	ABM00849	Human sec
843	6	4.5	453	6	ABO07753	Human PRO	916	6	4.5	453	6	ABR88451	Human sec
844	6	4.5	453	6	ABR69994	Human sec	917	6	4.5	453	6	ABM77272	Human sec
845	6	4.5	453	6	ABR69327	Human sec	918	6	4.5	453	6	ABO28756	Human sec
846	6	4.5	453	6	ABO01468	Human PRO	919	6	4.5	453	6	ABO31501	Human sec
847	6	4.5	453	6	ABU81270	Human PRO	920	6	4.5	453	6	ABM07918	Human sec
848	6	4.5	453	6	ABR60067	Human sec	921	6	4.5	453	6	ABO40398	Human sec
849	6	4.5	453	6	ABR67802	Human sec	922	6	4.5	453	6	ABO35823	Human PRO
850	6	4.5	453	6	ABR65190	Human sec	923	6	4.5	453	6	ABO43962	Human PRO
851	6	4.5	453	6	ABR68412	Human sec	924	6	4.5	453	6	ADA77816	Human sec
852	6	4.5	453	6	ABR71824	Human sec	925	6	4.5	453	6	ABM24757	Human sec
853	6	4.5	453	6	ABU85304	Human PRO	926	6	4.5	453	6	ABO03025	Human sec
854	6	4.5	453	6	ABU88994	Human sec	927	6	4.5	453	6	ABR90281	Human sec
855	6	4.5	453	6	ABU83074	Human sec	928	6	4.5	453	6	ABM17195	Human sec
856	6	4.5	453	6	ABU94930	Novel hum	929	6	4.5	453	6	ABU62146	Tumour-ab
857	6	4.5	453	6	ABU90478	Novel hum	930	6	4.5	453	6	ABR94941	Human sec
858	6	4.5	453	6	ABU83989	Human sec	931	6	4.5	453	6	ABR95246	Human sec
859	6	4.5	453	6	ABU93640	Novel hum	932	6	4.5	453	6	ABO21484	Human sec
860	6	4.5	453	6	ABR64885	Human sec	933	6	4.5	453	6	ABR97748	Human sec
861	6	4.5	453	6	ABR68717	Human sec	934	6	4.5	453	6	ABR87536	Human sec
862	6	4.5	453	6	ABO06533	Human sec	935	6	4.5	453	6	ABM77577	Human sec
863	6	4.5	453	6	ABR99078	Human sec	936	6	4.5	453	6	ABM27807	Human sec
864	6	4.5	453	6	ABU56962	Human PRO	937	6	4.5	453	6	ABM06088	Human sec
865	6	4.5	453	6	ABU85914	Novel hum	938	6	4.5	453	6	ABM03594	Human sec
866	6	4.5	453	6	ABU82201	Novel hum	939	6	4.5	453	6	ABM35045	Human sec
867	6	4.5	453	6	ABU87212	Human PRO	940	6	4.5	453	6	ABM26282	Human sec
868	6	4.5	453	6	ABU83684	Human sec	941	6	4.5	453	6	ABO48064	Human sec
869	6	4.5	453	6	ABO08058	Human PRO	942	6	4.5	453	6	ABR92806	Human sec
870	6	4.5	453	6	ABU81769	Novel hum	943	6	4.5	453	6	ABO24567	Human sec
871	6	4.5	453	6	ABU65933	Novel hum	944	6	4.5	453	6	ABM11578	Human sec
872	6	4.5	453	6	ABR59762	Human sec	945	6	4.5	453	6	ABM02679	Human sec
873	6	4.5	453	6	ABU93950	Novel hum	946	6	4.5	453	6	ABM15975	Human sec
874	6	4.5	453	6	ABU80349	Human sec	947	6	4.5	453	6	ABO27536	Human sec
875	6	4.5	453	6	ABU99803	Novel hum	948	6	4.5	453	6	ABM29027	Human sec
876	6	4.5	453	6	ABR66473	Human sec	949	6	4.5	453	6	ABM07003	Human sec
877	6	4.5	453	6	ABR90891	Human sec	950	6	4.5	453	6	ABM21097	Human sec
878	6	4.5	453	6	ABU94318	Human PRO	951	6	4.5	453	6	ABM09443	Human sec
879	6	4.5	453	6	ABU79200	Human PRO	952	6	4.5	453	6	ABO41313	Human sec
880	6	4.5	453	6	ABU86529	Human sec	953	6	4.5	453	6	ABO36128	Human PRO
881	6	4.5	453	6	ABU86834	Novel hum	954	6	4.5	453	6	ABO43657	Human PRO
882	6	4.5	453	6	ABU94623	Human PRO	955	6	4.5	453	6	ABM76357	Human sec
883	6	4.5	453	6	ABO04550	Human PRO	956	6	4.5	453	6	ABM76053	Human sec
884	6	4.5	453	6	ABR70299	Human sec	957	6	4.5	453	6	ABM25672	Human sec
885	6	4.5	453	6	ABU98464	Human PRO	958	6	4.5	453	6	ABM25977	Human sec
886	6	4.5	453	6	ABR65863	Human sec	959	6	4.5	453	6	ABO03330	Human sec
887	6	4.5	453	6	ABR64580	Human sec	960	6	4.5	453	6	ABO02415	Human sec
888	6	4.5	453	6	ABU79505	Human PRO	961	6	4.5	453	6	ABR90586	Human sec
889	6	4.5	453	6	ABU92896	Human sec	962	6	4.5	453	6	ABR73654	Human sec
890	6	4.5	453	6	ABU95855	Human PRO	963	6	4.5	453	6	ABO16906	Human sec
891	6	4.5	453	6	ABU91075	Novel hum	964	6	4.5	453	6	ABR94331	Human sec
892	6	4.5	453	6	ABU90168	Novel hum	965	6	4.5	453	6	ABR75838	Human sec
893	6	4.5	453	6	ABO09583	Human sec	966	6	4.5	453	6	ABR71214	Human sec
894	6	4.5	453	6	ABO10855	Human sec	967	6	4.5	453	6	ABR93111	Human sec
895	6	4.5	453	6	ABR70909	Human sec	968	6	4.5	453	6	ABR93416	Human sec
896	6	4.5	453	6	ABU87517	Human PRO	969	6	4.5	453	6	ABR87841	Human sec
897	6	4.5	453	6	ABU91385	Human PRO	970	6	4.5	453	6	ABO27841	Human sec
898	6	4.5	453	6	ABU84599	Human sec	971	6	4.5	453	6	ABO29976	Human sec
899	6	4.5	453	6	ABR69689	Human sec	972	6	4.5	453	6	ABO33185	Human PRO
900	6	4.5	453	6	ABU80066	Human PRO	973	6	4.5	453	6	ABM04873	Human sec
901	6	4.5	453	6	ABU93335	Human PRO	974	6	4.5	453	6	ABM08833	Human sec

975 6 4.5 453 6 ABO36433 Human sec
 976 6 4.5 453 6 ABO35518 Human PRO
 977 6 4.5 453 6 ABO39483 Human sec
 978 6 4.5 453 6 ABO10358 Human sec
 979 6 4.5 453 6 ABO11883 Human sec
 980 6 4.5 453 6 ABO52029 Human PRO
 981 6 4.5 453 6 ABO52334 Human PRO
 982 6 4.5 453 6 ABO23652 Human sec
 983 6 4.5 453 6 ABR97138 Human sec
 984 6 4.5 453 6 ABR86926 Human sec
 985 6 4.5 453 6 ABO10968 Human sec
 986 6 4.5 453 6 ABO28112 Human sec
 987 6 4.5 453 6 ABO32111 Human sec
 988 6 4.5 453 6 ABO15238 Human sec
 989 6 4.5 453 6 ABO06393 Human sec
 990 6 4.5 453 6 ABO04204 Human sec
 991 6 4.5 453 6 ABO07613 Human sec
 992 6 4.5 453 6 ABO07613 Human sec
 993 6 4.5 453 6 ABO40703 Human sec
 994 6 4.5 453 6 ABO35350 Human sec
 995 6 4.5 453 6 ABO33113 Human sec
 996 6 4.5 453 6 ABO52639 Human PRO
 997 6 4.5 453 6 ABO50199 Human sec
 998 6 4.5 453 6 ABO99193 Human sec
 999 6 4.5 453 6 ABO04245 Human sec
 1000 6 4.5 453 6 ABO05875 Human sec

ALIGNMENTS

RESULT 1
 AAE03669
 ID AAE03669 standard; protein; 132 AA.
 XX
 AC AAE03669;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human SPOD TRAF-protein binding domain (TPBD) protein #3.
 XX
 KW Human; speckle-type POZ protein; SPOD; therapy; tumour necrosis factor;
 KW TNF receptor-associated factor; adenocarcinoma; autoimmune disease;
 KW TRAF-protein binding domain; TPBD; allergy; cancer; allograft rejection;
 KW sepsis; glioma; carcinoma; sarcoma; melanoma; hamartoma; leukaemia;
 KW lymphoma; neoplasia; benign proliferative disease; restenosis; fibrosis;
 KW keratinocyte hyperplasia; benign prostatic hypertrophy; keloid;
 KW inflammatory hyperplasia; balloon angioplasty; bone marrow aplasia;
 KW stress response; cellular proliferation; immunoglobulin class switching;
 KW Ig; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200132696-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US030533.
 XX
 PR 05-NOV-1999; 99US-00434784.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 FI Zapata JM, Reed JC;
 XX
 DR WPI; 2001-381115/40.
 XX
 PT New TRAF-protein binding domain polypeptide, useful e.g. for treatment
 PT and diagnosis of cancer or autoimmune diseases, also related nucleic acid
 PT and modulators.
 XX
 PS Claim 4; Page 146-147; 156pp; English.
 XX

CC The present sequence is human speckle-type POZ protein (SPOD) TRAF
 CC domain (TPBD) protein. TPBDs and/or anti-TPBD antibodies (Ab) are used to
 CC identify agents for treatment of autoimmune diseases, inflammation,
 CC allergy, allograft rejection, sepsis, cancers such as gliomas,
 CC carcinomas, adenocarcinomas, sarcomas, melanomas, hamartomas, leukaemias
 CC and lymphomas, benign proliferative diseases, benign prostatic
 CC hyperplasia, keratinocyte hyperplasia, neoplasia, keloid, inflammatory
 CC hyperplasia, fibrosis, smooth muscle cell proliferation in arteries
 CC following balloon angioplasty (restenosis), bone marrow aplasia or
 CC generally any condition that involves abnormal apoptosis, cellular
 CC proliferation, differentiation or stress responses or immunoglobulin
 CC class switching in B cells. Agents (Ab or oligonucleotides) that bind
 CC specifically to TPBD or its nucleic acid are useful for diagnosis of the
 CC specified diseases, particularly for diagnosis or prognosis of cancer or
 CC for monitoring therapy
 XX
 SQ Sequence 132 AA;
 Query Match 100.0%; Score 132; DB 4; Length 132;
 Best Local Similarity 100.0%; Pred. No. 1.8e-137;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 SYWMTINNFSFCREEMGEVIKSTFFSGANDKLKWLCLRVNPKGLDESKDYLSYLLVLS 60
 Db 1 SYWMTINNFSFCREEMGEVIKSTFFSGANDKLKWLCLRVNPKGLDESKDYLSYLLVLS 60
 Oy 61 CPKSEVRVKFKFSILNAKBETKAMESQRAYRFVQKDWGFKKFIIRDLLDEANGLLPD 120
 Db 61 CPKSEVRVKFKFSILNAKBETKAMESQRAYRFVQKDWGFKKFIIRDLLDEANGLLPD 120
 Oy 121 DKLTLCFCEVSVV 132
 Db 121 DKLTLCFCEVSVV 132
 RESULT 2
 AAE03662
 ID AAE03662 standard; protein; 180 AA.
 XX
 AC AAE03662;
 XX
 DT 29-AUG-2001 (first entry)
 XX
 DE Human SPOD TRAF-protein binding domain (TPBD) protein #2.
 XX
 KW Human; speckle-type POZ protein; SPOD; therapy; tumour necrosis factor;
 KW TNF receptor-associated factor; adenocarcinoma; autoimmune disease;
 KW TRAF-protein binding domain; TPBD; allergy; cancer; allograft rejection;
 KW sepsis; glioma; carcinoma; sarcoma; melanoma; hamartoma; leukaemia;
 KW lymphoma; neoplasia; benign proliferative disease; restenosis; fibrosis;
 KW keratinocyte hyperplasia; benign prostatic hypertrophy; keloid;
 KW inflammatory hyperplasia; balloon angioplasty; bone marrow aplasia;
 KW stress response; cellular proliferation; immunoglobulin class switching;
 KW Ig; apoptosis.
 XX
 OS Homo sapiens.
 XX
 PN WO200132696-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US030533.
 XX
 PR 05-NOV-1999; 99US-00434784.
 XX
 PA (BURN-) BURNHAM INST.
 XX
 FI Zapata JM, Reed JC;
 XX
 DR WPI; 2001-381115/40.
 DR N-PSDB; AAD08070.
 XX

PT New TRAF-protein binding domain polypeptide, useful e.g. for treatment
PT and diagnosis of cancer or autoimmune diseases, also related nucleic acid
PT and modulators.

PS Claim 4; Page 131-132; 156pp; English.

XX The present sequence is human speckle-type POZ protein (SPOP) TRAF
CC (tumour necrosis factor, TNF receptor-associated factor)-protein binding
CC domain (TPBD) protein. TPBDs and/or anti-TPBD antibodies (Ab) are used to
CC identify agents for treatment of autoimmune diseases, inflammation,
CC allergy, allograft rejection, sepsis, cancers such as gliomas, leukaemias
CC carcinomas, adenocarcinomas, sarcomas, melanomas, hamartomas, benign
CC and lymphomas, benign proliferative diseases, benign prostatic
CC hyperplasia, keratinocyte hyperplasia, neoplasia, keloid, inflammatory
CC following balloon angioplasty (restenosis), bone marrow aplasia or
CC generally any condition that involves abnormal apoptosis, cellular
CC proliferation, differentiation or stress responses or immunoglobulin
CC class switching in B cells. Agents (Ab or oligonucleotides) that bind
CC specifically to TPBD or its nucleic acid are useful for diagnosis of the
CC specified diseases, particularly for diagnosis or prognosis of cancer or
CC for monitoring therapy

XX SQ Sequence 180 AA;

Query Match 100.0%; Score 132; DB 4; Length 180;
Best Local Similarity 100.0%; Pred. No. 2.5e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREMGEVKSSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 60
Db 33 SYMTINNFSFCREMGEVKSSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 92
Qy 61 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db 93 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164

RESULT 3
AAB90799
ID AAB90799 standard; protein; 374 AA.

AC AAB90799;
XX 15-JUN-2001 (first entry)
DT Human shear stress-response protein SEQ ID NO: 98.

XX Human; shear stress-response protein; vascular disease; arteriosclerosis.

XX Homo sapiens.

OS WO200125427-A1.

PN 12-APR-2001.

PD 02-OCT-2000; 2000WO-JP006840.

PF 01-OCT-1999; 93JP-00280976.

PR (KYOW) KYOWA HAKKO KOGYO KK.

XX (NOJI/) NOJIMA H.

PI Nojima H, Yoshie H, Obayashi M, Ota T, Kawabata A, Sakurada K;

PI Kuga T, Sekine S, Nakamura Y, Sugano S;

XX WPI; 2001-266308/27.

DR N-PSDB; AAB02922.

PT DNA sequences, proteins encoded by them and antibodies against them
PT useful in diagnosis and treatment of vascular disease caused by
PT arteriosclerosis.

PS Claim 60; Page 503-505; 678pp; Japanese.

XX The present invention provides the protein and coding sequences of a
CC number of human shear stress response proteins. These are useful in the
CC diagnosis, treatment and screening of vascular diseases caused by
CC arteriosclerosis, including heart failure, post-PTCA restenosis and
CC hypertension

XX SQ Sequence 374 AA;

Query Match 100.0%; Score 132; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREMGEVKSSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 60
Db 33 SYMTINNFSFCREMGEVKSSTFSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 92
Qy 61 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db 93 CPKSEVRKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164

RESULT 4

AAB03659

ID AAB03659 standard; protein; 374 AA.

XX AAB03659;

XX 29-AUG-2001 (first entry)

DT Human SPOP TRAF-protein binding domain (TPBD) protein #1.

XX Human; speckle-type POZ protein; SPOP; therapy; tumour necrosis factor;
XX TNF receptor-associated factor; adenocarcinoma; autoimmune disease;
XX TRAF-protein binding domain; TPBD; allergy; cancer; allograft rejection;
XX sepsis; glioma; carcinoma; sarcoma; melanoma; hamartoma; leukaemia;
XX lymphoma; neoplasia; benign proliferative disease; restenosis; fibrosis;
XX keratinocyte hyperplasia; benign prostatic hypertrophy; keloid;
XX inflammatory hyperplasia; balloon angioplasty; bone marrow aplasia;
XX stress response; cellular proliferation; immunoglobulin class switching;
XX Ig; apoptosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 1..180

FT /note= "TRAF-protein binding domain fragment"

PN WO200132696-A2.

XX 10-MAY-2001.

XX 03-NOV-2000; 2000WO-US030533.

XX 05-NOV-1999; 99US-00434784.

XX (BURN-) BURNHAM INST.

XX Zapata JM, Reed JC;

XX WPI; 2001-381115/40.

DR N-PSDB; AAD08067.

XX New TRAF-protein binding domain polypeptide, useful e.g. for treatment

PT and diagnosis of cancer or autoimmune diseases, also related nucleic acid
PT and modulators.

PS Claim 57; Page 116-117; 156pp; English.

XX The present sequence is human speckle-type POZ protein (SPOP) TRAF
CC (tumour necrosis factor, TNF receptor-associated factor)-protein binding
CC domain (TPBD). TPBDs and/or anti-TPBD antibodies (Ab) are used to
CC identify agents for treatment of autoimmune diseases, inflammation,
CC allergy, allograft rejection, sepsis, cancers such as gliomas,
CC carcinomas, adenocarcinomas, sarcomas, melanomas, hamartomas, leukaemias
CC and lymphomas, benign proliferative diseases, benign prostatic
CC hypertrophy, keratinocyte hyperplasia, neoplasia, keloid, inflammatory
CC hyperplasia, fibrosis, smooth muscle cell proliferation in arteries
CC following balloon angioplasty (restenosis), bone marrow aplasia or
CC generally any condition that involves abnormal apoptosis, cellular
CC proliferation, differentiation or stress responses or immunoglobulin
CC class switching in B cells. Agents (Ab or oligonucleotides) that bind
CC specifically to TPBD or its nucleic acid are useful for diagnosis of the
CC specified diseases, particularly for diagnosis or prognosis of cancer or
CC for monitoring therapy

XX Sequence 374 AA;

Query Match 100.0%; Score 132; DB 4; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 60
DB 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 92
QY 61 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLPD 120
DB 93 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLPD 152
QY 121 DKLTLCFCEVSVV 132
DB 153 DKLTLCFCEVSVV 164

RESULT 5
ADB85287
ID ADB85287 standard; protein; 374 AA.

XX ADB85287;

XX 04-DEC-2003 (first entry)

XX Human prosaposin SEQ ID NO:168.

XX rat; streptozocin; kinase; phosphatase; ion channel protein; receptor;
KW transporter; G-protein coupled receptor; GPCR; DNA-binding proteins;
KW protease; enzyme; analgesic; gene therapy; pain; diabetes.

XX Rattus norvegicus.

XX EP1284297-A2.

XX 19-FEB-2003.

XX 26-JUL-2002; 2002EP-00255228.

XX 27-JUL-2001; 2001GB-00018354.

XX 07-FEB-2002; 2002GB-00002880.

XX (WARN) WARNER LAMBERT CO.

XX Brooksbank RA, Dixon AK, Lee K, Pinnock RD;

XX WPI; 2003-364994/35.

XX N-PSDB; ADB85288.

PT Use of gene sequence that is down-regulated in response to streptozocin-
PT induced diabetes, vector, host cell, animal, polypeptide and antibody, in
XX screening of compounds for treating or diagnosing pain.

XX Disclosure; Page 243-244; 256pp; English.

PS The invention relates to a novel isolated gene sequence that is down-
CC regulated in the spinal cord in response to streptozocin-induced
CC diabetes, or comprising, hybridising or having at least 80% sequence
CC identity to a sequence whose expression products are kinases,
CC phosphatases, ion channel proteins, receptors, transporters, G-protein
CC coupled receptor proteins, DNA-binding proteins, proteases or enzymes,
CC given in the specification. A gene of the invention has analgesic
CC activity, and may have a use in gene therapy. The gene sequences, vector,
CC host cell, animal, polypeptide and antibody are useful for screening of
CC compounds for diagnosing or treating pain. The kits are useful for
CC simultaneous, separate or sequential detecting and/or quantifying down-
CC regulation of a gene sequence in the spinal cord of a mammal in response
CC to streptozocin-induced diabetes. The compound or pharmaceutical
CC composition is useful as a medicament for treating or diagnosing pain.
CC The present sequence represents a protein encoded by a gene of the
CC invention.

XX Sequence 374 AA;

Query Match 100.0%; Score 132; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 60
DB 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLLVLS 92
QY 61 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLPD 120
DB 93 CPKSEVRAKFKFSILNAKGEETKAMESQRAYRFVQGDWGFKKFIRRDFLDEANGLLPD 152
QY 121 DKLTLCFCEVSVV 132
DB 153 DKLTLCFCEVSVV 164

RESULT 6
ADI62718
ID ADI62718 standard; protein; 374 AA.

XX ADI62718;

XX 22-APR-2004 (first entry)

XX Human apoptosis-associated protein SEQ ID 161.

XX apoptosis; cell death; cytostatic; neuroprotective; immunosuppressive;
KW antirheumatic; antilathritic; dermatological; antiinflammatory;
KW hepatotropic; virucide; nontropic; anticonvulsant; antiparkinsonian;
KW vasotropic; cerebroprotective; antialcoholic; gene therapy; tumour;
KW autoimmune disease; degenerative disease; viral infection; leukaemia;
KW carcinoma; sarcoma; multiple sclerosis; rheumatoid arthritis; diabetes;
KW lupus; hepatitis; influenza viruses; Alzheimer's disease;
KW Huntington's disease; Parkinson's diseases; reperfusion injury; stroke;
KW alcoholic liver disease; human.

XX Homo sapiens.

XX WO2003058021-A2.

XX 17-JUL-2003.

XX 13-JAN-2003; 2003WO-EP000270.

XX 11-JAN-2002; 2002DE-01000856.

XX (XANT-) XANTOS BIOMEDICINE AG.

XX Koenig-Hoffman K, Kazinski M, Schaefer R, Kesper B;
PI WPI; 2003-542134/51.
XX N-PSDB; ADI62616.
DR
XX
PT New nucleic acids involved in apoptosis, useful for diagnosis and
FT treatment of e.g. tumors and degenerative disease, also related proteins,
PT antibodies and modulators.
XX
XX
PS Claim 1a; SEQ ID NO 161; 517pp; German.
XX
XX This invention describes novel nucleic acid molecules that are associated
CC with apoptosis and encode a polypeptide and are derived from a normalised
CC gene library (embryonic or liver) or clone collections, and the extent of
CC apoptosis measured by cell death detection assay or the CPRG assay
CC (measuring loss of membrane integrity). The products of the invention
CC have cytostatic, neuroprotective, immunosuppressive, antineoplastic,
CC antiarthritic, dermatological, antiinflammatory, hepatotropic, virucide,
CC nootropic, anticonvulsant, antiparkinsonian, vasotropic,
CC cerebroprotective and antialcoholic activity and can be used for gene
CC therapy. The polynucleotides also related vectors, hosts (or their
CC extracts), encoded polypeptide (or their receptors) and/or agents that
CC inhibit their activity (including antisense sequences) are used for
CC treatment or prevention of tumours, autoimmune or degenerative diseases
CC and viral infections, specifically leukaemia, carcinoma, sarcoma,
CC multiple sclerosis, rheumatoid arthritis, diabetes, lupus, or infection
CC with hepatitis or influenza viruses, Alzheimer's, Huntington's or
CC Parkinson's diseases, reperfusion injury, stroke and alcoholic liver
CC disease. Detection of the polynucleotides and derived polypeptides can
CC also be used for diagnosis of these diseases. This sequence represents an
CC apoptosis-associated protein described in the invention.
XX
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 132; DB 7; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 60
Db 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 92

Qy 61 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 120
Db 93 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 152

Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164

RESULT 7
ADQ89936
ID ADQ89936 standard; protein; 374 AA.
XX
XX
AC ADQ89936;
XX
XX 21-OCT-2004 (first entry)
XX
XX Antagonist of cell cycle progression polypeptide #183.
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX
XX Homo sapiens.
XX
XX WO2004063362-A2.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.
XX
XX
XX
XX

PR 10-JAN-2003; 2003US-0439123P.
XX 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
XX
XX Glover D, Bell G, Frenz L, Midgley C;
PI WPI; 2004-544089/52.
XX N-PSDB; ADQ89935.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
FT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 366; 461pp; English.
XX
XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
CC sequence.
XX
XX
SQ Sequence 374 AA;

Query Match 100.0%; Score 132; DB 8; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 60
Db 33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDESKDYLSLYLLVLS 92

Qy 61 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 120
Db 93 CPKSEVRAPKFSILNAKGETKAMESORAYRFVQGDWGFKFIIRDFLLDEANGLLPD 152

Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164

RESULT 8
ADQ89928
ID ADQ89928 standard; protein; 374 AA.
XX
XX
AC ADQ89928;
XX
XX 21-OCT-2004 (first entry)
XX
XX Antagonist of cell cycle progression polypeptide #179.
XX
XX Cytostatic; cancer; cell division cycle; mitosis; meiosis;
KW cell cycle progression.
XX
XX Homo sapiens.
XX
XX WO2004063362-A2.
XX
XX 29-JUL-2004.
XX
XX 31-DEC-2003; 2003WO-GB005635.
XX
XX
XX
XX 10-JAN-2003; 2003US-0439123P.
XX 06-MAY-2003; 2003US-0468402P.
XX
XX (CYCL-) CYCLACEL LTD.
XX

XX
PI Glover D, Bell G, Frenz L, Midgley C;
XX WPI; 2004-544089/52.
DR N-PSDB; AD089927.
XX
XX New cell cycle progression genes and proteins for modulating cell cycle
PT progression in cells, for preventing, treating or diagnosing cell
PT proliferative diseases (e.g. cancer) or for identifying modulators of
PT mitosis or meiosis.
XX
XX Claim 2; SEQ ID NO 358; 461pp; English.
PS
XX The present invention relates to a polynucleotide for preventing,
CC treating or diagnosing a disease in an individual. The composition or the
CC polypeptide, polynucleotide or RNA precursor, or antibody is useful for
CC diagnosing, preventing or treating diseases (e.g. cell proliferative
CC diseases such as cancer) in an individual. These may also be used for
CC identifying substances capable of binding to or modulating the function
CC of the polypeptide, capable of affecting the function of the
CC corresponding gene, or capable of inhibiting the cell division cycle or
CC cell cycle progression, preferably mitosis and/or meiosis. The present
CC sequence represents an antagonist of cell cycle progression protein
XX
XX Sequence 374 AA;
SQ
Query Match 100.0%; Score 132; DB 8; Length 374;
Best Local Similarity 100.0%; Pred. No. 4.9e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCEEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLVLS 60
Db 33 SYMTINNFSFCEEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLVLS 92
Qy 61 CPKSEVRAKFKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db 93 CPKSEVRAKFKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 152
Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164
RESULT 9
AAB58286
ID AAB58286 standard; protein; 395 AA.
AC AAB58286;
XX
XX 14-MAR-2001 (first entry)
XX
XX Lung cancer associated polypeptide sequence SEQ ID 624.
XX
XX Human; lung cancer associated protein; neuroprotective; cytoskeletal;
KW cardiac; immunomodulatory; muscular active; vulnerable;
KW gastrointestinal; nephrotropic; anti-infective; gynecological;
KW antibacterial; diagnosis; neural disorder; immune disorder; reproductive;
KW proliferative disorder; wound healing; infectious disease.
XX
XX Homo sapiens.
XX
XX WO200055180-A2.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US005918.
XX
XX 12-MAR-1999; 99US-0124270P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
PA (ROSE/) ROSEN C A.
XX

PI Ruben SM;
XX
XX WPI; 2000-587514/55.
DR N-PSDB; AAF18162.
XX
XX Lung cancer associated gene sequences, referred to as lung cancer
PT antigens, useful for treatment, prevention, and diagnosis of disorders
PT such as lung cancer.
XX
XX Claim 11; Page 1117-1119; 1425pp; English.
PS
XX Polynucleotide sequences AAF17982 - AAF18424 encode human lung cancer
CC associated proteins represented in AAB58106 - AAB58548. Lung cancer
CC associated proteins and polynucleotide sequences, their agonists, and
CC immunomodulators may have neuroprotective; cytoskeletal; cardiac;
CC general; nephrotropic; anti-infective; gynecological; or antibacterial
CC activity. The invention also includes antibodies specific for the protein
CC or polynucleotide sequences. The lung cancer associated polynucleotide
CC sequences may be used for detection of lung cancer, chromosome
CC identification, as chromosome markers, and for numerous other diagnostic
CC or research purposes. The proteins may be used to treat disorders such as
CC neural, immune, muscular, reproductive, gastrointestinal, pulmonary,
CC cardiovascular, renal, and proliferative disorders. The proteins may also
CC be used in the treatment of wounds and infectious diseases.
CC Polynucleotide sequences AAF18425 - AAF18433 and peptide AAB58549 are
CC used in the course of the invention for the identification and
CC characterisation of the polynucleotide and protein sequences
XX
XX Sequence 385 AA;
SQ
Query Match 100.0%; Score 132; DB 3; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.1e-137;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCEEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLVLS 60
Db 44 SYMTINNFSFCEEMGEVSKSTFSSGANDKLKWLVRNPKGLDESKDYLISYLLVLS 103
Qy 61 CPKSEVRAKFKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 120
Db 104 CPKSEVRAKFKFSILNAKGETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPD 163
Qy 121 DKLTLCFCEVSVV 132
Db 164 DKLTLCFCEVSVV 175
RESULT 10
ABG23713
ID ABG23713 standard; protein; 398 AA.
XX
XX ABG23713;
XX
XX 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #23704.
XX
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
XX Homo sapiens.
XX
XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US008631.
XX
XX 31-MAR-2000; 2000US-00540217.
PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
PA

CC supplements. These are useful in gene therapy, particularly for treating
CC wounds, burns or ulcers, Alzheimer's disease, Huntington's disease,
CC amyotrophic lateral sclerosis, autoimmune disorders, cancer or
CC inflammation. The nucleic acids and polypeptides are also useful in
CC diagnostic and research methods. The sequences given in records ABP43544-
CC ABP43989 represent polypeptides encoded by polynucleotides of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 392 AA;

Query Match 40.2%; Score 53; DB 5; Length 392;
Best Local Similarity 100.0%; Pred. No. 1.3e-49;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 132
|||||
Db 112 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 164

RESULT 15

ABU96687
ID ABU96687 standard; protein; 392 AA.

XX AC ABU96687;

DT 25-JUL-2003 (first entry)

XX DE Human nucleic acid-associated protein (NAAP) #16.

XX KW Human; nucleic acid-associated protein; cytostatic; antiarteriosclerotic;
XX KW anticonvulsant; nootropic; neuroprotective; cerebroprotective; anti-HIV;
XX KW anti-allergic; anti-inflammatory; thymimetic; gene therapy;
XX KW cell proliferative disorder; cancer; atherosclerosis;
XX KW neurological disorder; epilepsy; Huntington's disease; stroke;
XX KW immune disorder; inflammatory disorder; AIDS; allergy;
XX KW developmental disorder; Hypothyroidism; Cushing's syndrome; infection;
XX KW protein-protein interaction; drug-target interaction;
XX KW gene expression profile.

XX OS Homo sapiens.

XX PN WO2003023003-A2.

XX XX 20-MAR-2003.

XX PF 05-SEP-2002; 2002WO-US028540.

XX PR 07-SEP-2001; 2001US-0317792P.

XX PR 07-SEP-2001; 2001US-0317912P.

XX PR 14-SEP-2001; 2001US-0322270P.

XX PR 21-SEP-2001; 2001US-0324040P.

XX PR 28-SEP-2001; 2001US-0326732P.

XX PR 19-OCT-2001; 2001US-0346716P.

XX PR 25-JAN-2002; 2002US-0351749P.

XX PR 22-FEB-2002; 2002US-0359498P.

XX XX (INCY-) INCYTE GENOMICS INC.

XX PI Tang Yt, Jackson JL, Griffin JA, Elliott VS, Forsythe IJ;

XX PI Becha SD, Richardson TW, Lee EA, Sprague WW, Emerling BM;

XX PI Thangavelu K, Warren EA, Tran UK, Yue H, Xu Y, Yue H, Li JX;

XX PI Hafalia AJA, Sarjanwala B, Marquis JP, Gorvad AE, Lee SY, Ison CH;

XX PI Baughn MR, Chawla NK, Nguyen DB, Swarnakar A, Zebardjian Y, Shah P;

XX PI Thornton M, Yao MG, Khan FA, Gandhi AR, Yang J, Kable AE;

XX PI Burford N, Ramkumar J;

PT aberrant NAAP expression e.g. cancer, AIDS, atherosclerosis, epilepsy, or
PT infections.

XX Claim 1; Page 253; 345pp; English.

XX CC The invention describes a novel human isolated nucleic acid-associated
CC polypeptide (NAAP). The polypeptides and polynucleotides are useful in
CC diagnosing, treating and preventing diseases or conditions associated
CC with the decreased expression or overexpression of NAAP, such as cell
CC proliferative (e.g. cancer, atherosclerosis), neurological (e.g.
CC epilepsy, Huntington's disease, stroke), immune/inflammatory (e.g. AIDS,
CC allergies) and developmental (e.g. Hypothyroidism, Cushing's syndrome),
CC disorders, or infections. These are also useful in assessing the effects
CC of exogenous compounds on the expression of nucleic acid and amino acid
CC sequences of NAAP. The NAAP or its fragments are useful in screening
CC compounds for effectiveness as agonist or antagonist of the polypeptides,
CC or in altering the expression of the target polynucleotide and compounds
CC that specifically bind to or modulate the activity of the polypeptide.
CC The microarray is useful in monitoring or measuring protein-protein
CC interactions, drug-target interactions, and gene expression profiles.

XX CC This is the amino acid sequence of a novel human nucleic acid-associated
CC protein (NAAP)

XX SQ Sequence 392 AA;

Query Match 40.2%; Score 53; DB 6; Length 392;

Best Local Similarity 100.0%; Pred. No. 1.3e-49;

Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 132
|||||
Db 112 EETKAMESQRAYRFVQKDWGFKFIRDRDFLLDEANGLLPDDKLTLCFESVW 164

Search completed: July 20, 2005, 20:47:39

Job time : 128.457 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:52:32 ; Search time 83.9143 Seconds
(without alignments)
610.633 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

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Gapop 60.0 , Gapext 60.0

Searched: 1736639 seqs, 388189149 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1736639

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*

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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pcp.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pcp.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pcp.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pcp.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pcp.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
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2	132	100.0	385 9	US-09-925-302-624
3	132	100.0	385 10	US-09-925-302-624
4	35	26.5	35 9	US-09-864-761-44291
5	33	25.0	195 9	US-09-764-864-1190
6	8	6.1	307 16	US-10-437-963-135131
7	7	5.3	46 14	US-10-201-444-7
8	7	5.3	59 16	US-10-425-115-266892
9	7	5.3	66 16	US-10-437-963-171570
10	7	5.3	71 15	US-10-424-599-264355
11	7	5.3	78 16	US-10-425-115-263100
Sequence 168, App				
Sequence 624, App				
Sequence 624, App				
Sequence 44291, A				
Sequence 1190, App				
Sequence 135131				
Sequence 7, Appli				
Sequence 266892,				
Sequence 171570,				
Sequence 264355,				
Sequence 263100,				

Sequence 357584,	US-10-425-115-357584	87	16
Sequence 170573,	US-10-437-963-170573	102	16
Sequence 361810,	US-10-425-115-361810	129	16
Sequence 44370, A	US-10-425-114-44370	146	15
Sequence 56, Appl	US-10-328-675A-56	165	14
Sequence 52, Appl	US-10-328-675A-52	166	14
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						Sequence 384, App							

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ALIGNMENTS

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; Publication No. US20030134301A1
; GENERAL INFORMATION:
; APPLICANT: Warner-Lambert Company
; APPLICANT: Lee, Kevin
; APPLICANT: Dixon, Alistair
; APPLICANT: Brooksbank, Robert
; APPLICANT: Pinnock, Robert
; TITLE OF INVENTION: Identification and Use of Molecules Implicated in Pain
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; CURRENT FILING DATE: 5200-07-24
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; FEATURE:
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Query Match 100.0%; Score 132; DB 14; Length 374;
Best Local Similarity 100.0%; Pred. No. 5.7e-125;

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Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRVNPVKGLDDESKDYLSYLLVLS 60
Db |||||
33 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRVNPVKGLDDESKDYLSYLLVLS 92
Qy 61 CPKSEVRKPKFSLNAKGETKAMESQRAYRFVQKDWGFKKFIIRDPLLDEANGLLPD 120
Db |||||
93 CPKSEVRKPKFSLNAKGETKAMESQRAYRFVQKDWGFKKFIIRDPLLDEANGLLPD 152
Qy 121 DKLTLCFCEVSV 132
Db |||||
153 DKLTLCFCEVSV 164

RESULT 2
US-09-925-302-624
; Sequence 624, Application US/09925302
; Patent No. US2002004941A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-302-624

Query Match 100.0%; Score 132; DB 9; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-125;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRVNPVKGLDDESKDYLSYLLVLS 60
Db |||||
44 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRVNPVKGLDDESKDYLSYLLVLS 103
Qy 61 CPKSEVRKPKFSLNAKGETKAMESQRAYRFVQKDWGFKKFIIRDPLLDEANGLLPD 120
Db |||||
104 CPKSEVRKPKFSLNAKGETKAMESQRAYRFVQKDWGFKKFIIRDPLLDEANGLLPD 163
Qy 121 DKLTLCFCEVSV 132
Db |||||
164 DKLTLCFCEVSV 175

RESULT 3
US-09-925-302-624
; Sequence 624, Application US/09925302
; Publication No. US20030064072A9
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA104
; CURRENT APPLICATION NUMBER: US/09/925,302
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05918
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 896
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 624
; LENGTH: 385
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-09-925-302-624

Query Match      100.0%; Score 132; DB 10; Length 385;
Best Local Similarity 100.0%; Pred. No. 5.9e-125; Mismatches 0; Indels 0; Gaps 0;
Matches 132; Conservative 0;

Qy 1 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDEESKDYLSLYLLVLS 60
    |||||||
Db 44 SYMTINNFSFCREEMGEVIKSTFSSGANDKLKWLVRNPKGLDEESKDYLSLYLLVLS 103
    |||||||

Qy 61 CPKSEVRAKFKPSILNAKEETKAMESQRAYRFVQGDWGFKKFIRRDFLDDEANGLLPDD 120
    |||||||
Db 104 CPKSEVRAKFKPSILNAKEETKAMESQRAYRFVQGDWGFKKFIRRDFLDDEANGLLPDD 163
    |||||||

Qy 121 DKTLFCEVSVV 132
    |||||||
Db 164 DKTLFCEVSVV 175
    |||||||

RESULT 4
US-09-864-761-44291
; Sequence 44291, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR FILING DATE: US 60/180,312
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 44291

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; LENGTH: 35
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC006487.7
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.77
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.79
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.68
; OTHER INFORMATION: EST HUMAN HIT: BE876686.1, EVALUE 3.00e-14
; OTHER INFORMATION: SWISSPROT HIT: O43791, EVALUE 2.00e-15
US-09-864-761-44291

Query Match      26.5%; Score 35; DB 9; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.2e-27;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 SQRAYRFVQGDWGFKKFIRRDFLDDEANGLLPDD 121
    |||||||
Db 1 SQRAYRFVQGDWGFKKFIRRDFLDDEANGLLPDD 35
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RESULT 5
US-09-764-864-1190
; Sequence 1190, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1190
; LENGTH: 195
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (171)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1190

Query Match      25.0%; Score 33; DB 9; Length 195;
Best Local Similarity 100.0%; Pred. No. 5.6e-25;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 100 GFKKFIRRDFLDDEANGLLPDDKLTLCFCEVSVV 132
    |||||||
Db 3 GFKKFIRRDFLDDEANGLLPDDKLTLCFCEVSVV 35
    |||||||

RESULT 6
US-10-437-963-135131
; Sequence 135131, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963

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nothing before 2000

; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 135131
; LENGTH: 307
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_36836C.1.pep
US-10-437-963-135131

Query Match 6.1%; Score 8; DB 16; Length 307;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGLL 118
| | | | |
Db 68 LDEANGLL 75

RESULT 7
US-10-201-444-7
; Sequence 7, Application US/10201444
; Publication No. US20030078378A1
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/10/201,444
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: US/08/861,476
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 46
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-201-444-7

Query Match 5.3%; Score 7; DB 14; Length 46;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 108 DFLDLEA 114
| | | | |
Db 29 DFLDLEA 35

RESULT 8
US-10-425-115-266892
; Sequence 266892, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 266892
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_175007C.1.pep
US-10-425-115-266892

Query Match 5.3%; Score 7; DB 16; Length 59;
Best Local Similarity 100.0%; Pred. No. 41;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 72 FSILNAK 78
| | | | |
Db 9 FSILNAK 15

RESULT 9
US-10-437-963-171570
; Sequence 171570, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 171570
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_6978C.1.pep
US-10-437-963-171570

Query Match 5.3%; Score 7; DB 16; Length 66;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 52 LSLYLLL 58
| | | | |
Db 13 LSLYLLL 19

RESULT 10
US-10-424-599-264355
; Sequence 264355, Application US/10424599
; Publication No. US2004031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264355
; LENGTH: 71
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_80733C.1.pep
US-10-424-599-264355

Query Match 5.3%; Score 7; DB 15; Length 71;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 SLYLLLV 59
| | | | |
Db 13 SLYLLLV 19

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RESULT 11
US-10-425-115-263100
; Sequence 263100, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 263100
; LENGTH: 78
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_17155C.1.pep
US-10-425-115-263100
Query Match          5.3%; Score 7; DB 16; Length 78;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 51 YLSLYLL 57
Db 54 YLSLYLL 60

RESULT 12
US-10-425-115-357584
; Sequence 357584, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 357584
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_89285C.1.pep
US-10-425-115-357584
Query Match          5.3%; Score 7; DB 16; Length 87;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 KSSTFSS 27
Db 78 KSSTFSS 84

RESULT 13
US-10-437-963-170573
; Sequence 170573, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
```

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; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 170573
; LENGTH: 102
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_68887C.1.pep
US-10-437-963-170573
Query Match          5.3%; Score 7; DB 16; Length 102;
Best Local Similarity 100.0%; Pred. No. 67;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 BETKAME 86
Db 33 BETKAME 39

RESULT 14
US-10-425-115-361810
; Sequence 361810, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 361810
; LENGTH: 129
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_93147C.1.pep
US-10-425-115-361810
Query Match          5.3%; Score 7; DB 16; Length 129;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 MGEVIKS 22
Db 69 MGEVIKS 75

RESULT 15
US-10-425-114-44370
; Sequence 44370, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
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; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 44370

; LENGTH: 146

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: 701169325_FLI.pcp

US-10-425-114-44370

Query Match 5.3%; Score 7; DB 15; Length 146;

Best Local Similarity 100.0%; Pred.No. 92;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 LLDKANG 116

|||||

Db 66 LLDKANG 72

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Job time : 97.9143 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:46 ; Search time 25.3929 Seconds
(without alignments)
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Perfect score: 135
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Gapop 60.0 , Gapext 60.0

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Minimum DB seq length: 0
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Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	7	5.2	133	4	US-09-270-767-35069	A	Sequence 35069, A
2	7	5.2	133	4	US-09-270-767-50286	A	Sequence 50286, A
3	7	5.2	138	4	US-09-902-540-13575	A	Sequence 13575, A
4	7	5.2	145	3	US-09-134-001C-5194	A	Sequence 5194, A
5	7	5.2	411	4	US-08-887-534A-80	Appl	Sequence 80, Appl
6	7	5.2	411	4	US-09-527-431-80	Appl	Sequence 80, Appl
7	7	5.2	411	4	US-09-446-861-80	Appl	Sequence 80, Appl
8	7	5.2	548	4	US-09-252-991A-20793	A	Sequence 20793, A
9	7	5.2	651	4	US-09-932-678-2	Appl	Sequence 2, Appl
10	6	4.4	36	4	US-09-902-540-16517	A	Sequence 16517, A
11	6	4.4	39	1	US-08-428-488-13	Appl	Sequence 13, Appl
12	6	4.4	41	2	US-08-960-022-12	Appl	Sequence 12, Appl
13	6	4.4	52	4	US-09-096-724B-32	Appl	Sequence 32, Appl
14	6	4.4	56	4	US-09-621-976-4130	Appl	Sequence 4130, Appl
15	6	4.4	60	4	US-09-248-796A-24792	A	Sequence 24792, A
16	6	4.4	63	4	US-09-480-297A-30	Appl	Sequence 30, Appl
17	6	4.4	69	4	US-09-328-352-4927	Appl	Sequence 4927, Appl
18	6	4.4	77	4	US-09-513-999C-6277	Appl	Sequence 6277, Appl
19	6	4.4	79	4	US-09-489-039A-11809	A	Sequence 11809, A
20	6	4.4	81	4	US-09-614-912-190	Appl	Sequence 190, Appl
21	6	4.4	100	4	US-09-513-999C-4768	Appl	Sequence 4768, Appl
22	6	4.4	112	4	US-09-513-999C-4379	Appl	Sequence 4379, Appl
23	6	4.4	132	4	US-09-513-999C-5589	Appl	Sequence 5589, Appl
24	6	4.4	132	4	US-09-513-999C-5590	Appl	Sequence 5590, Appl
25	6	4.4	132	4	US-09-513-999C-5591	Appl	Sequence 5591, Appl
26	6	4.4	140	4	US-09-252-991A-16605	Appl	Sequence 16605, A
27	6	4.4	141	4	US-09-621-976-6981	Appl	Sequence 6981, A

141	4	US-09-621-976-6982	Sequence 6982, Ap
141	4	US-09-513-999C-7895	Sequence 7895, Ap
142	4	US-09-216-393B-24	Sequence 24, Appl
166	4	US-09-621-976-5267	Sequence 5267, Ap
171	4	US-09-902-540-16814	Sequence 16814, A
175	4	US-09-134-000C-5373	Sequence 5373, Ap
181	4	US-09-710-279-86	Sequence 86, Appl
182	3	US-09-134-001C-3742	Sequence 3742, Ap
184	4	US-09-489-039A-7611	Sequence 7611, Ap
208	4	US-09-328-352-4746	Sequence 4746, Ap
209	4	US-09-096-724B-8	Sequence 8, Appl
209	4	US-09-096-724B-24	Sequence 24, Appl
215	4	US-09-252-991A-18224	Sequence 18224, A
215	4	US-09-538-092-39	Sequence 39, Appl
222	4	US-09-710-279-128	Sequence 128, Appl
225	4	US-09-252-991A-17464	Sequence 17464, A
225	4	US-09-270-767-38019	Sequence 38019, A
225	4	US-09-270-767-53236	Sequence 53236, A
227	4	US-09-248-796A-17491	Sequence 17491, A
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234	4	US-09-949-016-6539	Sequence 6539, Ap
241	4	US-09-252-991A-18244	Sequence 18244, A
244	4	US-09-489-039A-9217	Sequence 9217, Ap
250	4	US-09-107-532A-4737	Sequence 4737, Ap
275	4	US-09-803-671B-5	Sequence 5, Appl
275	4	US-10-274-409-5	Sequence 5, Appl
276	4	US-09-252-991A-18006	Sequence 18006, A
276	4	US-09-489-039A-9409	Sequence 9409, Ap
290	4	US-09-270-767-39231	Sequence 39231, A
290	4	US-09-270-767-54448	Sequence 54448, A
291	4	US-09-252-991A-28755	Sequence 28755, A
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296	4	US-09-711-164-327	Sequence 327, Appl
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302	4	US-09-489-039A-8608	Sequence 8608, Ap
304	4	US-09-248-796A-16929	Sequence 16929, A
306	1	US-08-217-327-6	Sequence 6, Appl
310	4	US-09-598-747-27	Sequence 27, Appl
311	4	US-09-489-039A-12640	Sequence 12640, A
312	4	US-09-949-016-8777	Sequence 8777, Ap
314	4	US-09-902-540-10356	Sequence 10356, A
315	4	US-09-252-991A-31850	Sequence 31850, A
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319	4	US-09-107-532A-5122	Sequence 5122, Ap
321	4	US-09-540-236-2542	Sequence 2542, Ap
321	4	US-09-248-796A-14683	Sequence 14683, A
324	3	US-09-134-001C-4080	Sequence 4080, Ap
325	4	US-09-252-991A-32561	Sequence 32561, A
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327	4	US-09-489-039A-9808	Sequence 9808, Ap
329	4	US-09-543-681A-5999	Sequence 5999, Ap
331	3	US-08-808-720-5	Sequence 5, Appl
331	4	US-09-467-638-5	Sequence 5, Appl
332	3	US-09-540-014-9	Sequence 9, Appl
332	4	US-10-091-841A-9	Sequence 9, Appl
339	4	US-09-438-185A-1049	Sequence 1049, Ap
345	4	US-09-538-092-588	Sequence 588, Appl
346	3	US-09-073-297-2	Sequence 2, Appl
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356	4	US-09-602-777A-424	Sequence 424, Appl
361	4	US-09-248-796A-16765	Sequence 16765, A
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393	4	US-09-902-540-10682	Sequence 10682, A
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395	3	US-08-476-900A-3	Sequence 3, Appl

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102	6	4.4	395	4	US-09-902-540-15474	Sequence 16474, A	175	6	4.4	601	4	US-09-903-012B-42	Sequence 42, Appli
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110	6	4.4	442	4	US-09-252-991A-26142	Sequence 26142, A	183	6	4.4	664	4	US-09-328-352-7056	Sequence 7056, Ap
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123	6	4.4	492	4	US-09-636-077A-19	Sequence 19, Appl	196	6	4.4	762	4	US-09-489-039A-10008	Sequence 10008, A
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127	6	4.4	492	4	US-09-636-596C-19	Sequence 19, Appl	200	6	4.4	853	3	US-08-699-103B-10	Sequence 10, Appl
128	6	4.4	492	4	US-10-023-894-20	Sequence 20, Appl	201	6	4.4	853	3	US-09-229-059-10	Sequence 10, Appl
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138	6	4.4	514	4	US-09-538-092-913	Sequence 913, App	211	6	4.4	946	4	US-09-657-931A-10	Sequence 10, Appl
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143	6	4.4	515	4	US-09-636-596C-6	Sequence 6, Appli	216	6	4.4	1036	3	US-08-953-823A-5	Sequence 5, Appli
144	6	4.4	515	4	US-10-023-894-18	Sequence 18, Appl	217	6	4.4	1036	4	US-09-398-239-5	Sequence 5, Appli
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267	6	4.4	3201	4	US-09-679-279-15	Sequence 15, Appl	340	5	3.7	23	4	US-09-576-824A-157	Sequence 157, App
268	6	4.4	3666	2	US-08-222-617A-12	Sequence 12, Appl	341	5	3.7	23	4	US-09-576-824A-157	Sequence 157, App
269	6	4.4	3727	2	US-08-222-617A-27	Sequence 27, Appl	342	5	3.7	24	1	US-08-218-025A-134	Sequence 134, App
270	6	4.4	3778	2	US-08-222-617A-2	Sequence 2, Appli	343	5	3.7	24	1	US-08-096-172A-6	Sequence 6, Appli
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272	5	3.7	8	3	US-08-756-849-120	Sequence 120, App	345	5	3.7	24	1	US-08-306-116A-16	Sequence 16, Appli
273	5	3.7	8	1	US-08-279-906A-12	Sequence 12, Appl	346	5	3.7	24	3	US-08-492-076-8	Sequence 8, Appli
274	5	3.7	8	1	US-08-279-906A-13	Sequence 13, Appl	347	5	3.7	24	3	US-08-492-076-8	Sequence 10, Appl
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279	5	3.7	9	3	US-08-756-849-117	Sequence 117, App	352	5	3.7	24	5	PCT-US94-08380-6	Sequence 6, Appli
280	5	3.7	9	3	US-08-756-849-119	Sequence 119, App	353	5	3.7	24	5	PCT-US94-08380-15	Sequence 15, Appl
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282	5	3.7	11	2	US-08-343-443B-66	Sequence 66, Appl	355	5	3.7	25	1	US-08-096-172A-24	Sequence 24, Appl
283	5	3.7	11	2	US-08-343-443B-76	Sequence 76, Appl	356	5	3.7	25	1	US-08-096-172A-33	Sequence 33, Appl
284	5	3.7	11	2	US-08-343-443B-82	Sequence 82, Appl	357	5	3.7	25	1	US-08-096-172A-38	Sequence 38, Appl
285	5	3.7	12	3	US-08-602-999A-272	Sequence 272, App	358	5	3.7	25	2	US-08-783-818-14	Sequence 14, Appl
286	5	3.7	12	4	US-09-500-124-272	Sequence 272, App	359	5	3.7	25	2	US-08-453-349-14	Sequence 14, Appl
287	5	3.7	14	1	US-07-756-250-14	Sequence 14, Appl	360	5	3.7	25	2	US-08-540-118-3	Sequence 3, Appli
288	5	3.7	14	3	US-08-949-059A-7	Sequence 7, Appli	361	5	3.7	25	2	US-08-146-028-11	Sequence 11, Appl
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290	5	3.7	15	1	US-08-279-906A-4	Sequence 4, Appli	363	5	3.7	25	2	US-08-146-028-115	Sequence 115, App
291	5	3.7	15	1	US-08-211-980-4	Sequence 4, Appli	364	5	3.7	25	2	US-08-146-028-157	Sequence 157, App
292	5	3.7	15	2	US-08-411-859-11	Sequence 11, Appl	365	5	3.7	25	2	US-08-447-214-2	Sequence 2, Appli
293	5	3.7	15	4	US-08-278-774-17	Sequence 17, Appl	366	5	3.7	25	2	US-08-979-385B-12	Sequence 12, Appl
294	5	3.7	15	5	PCT-US92-07111-4	Sequence 4, Appli	367	5	3.7	25	3	US-08-723-425A-11	Sequence 11, Appl
295	5	3.7	15	5	PCT-US93-07967-4	Sequence 4, Appli	368	5	3.7	25	3	US-08-723-425A-114	Sequence 114, App
296	5	3.7	16	1	US-07-756-250-4	Sequence 4, Appli	369	5	3.7	25	3	US-08-723-425A-115	Sequence 115, App
297	5	3.7	16	2	US-08-433-133-97	Sequence 97, Appl	370	5	3.7	25	3	US-08-723-425A-157	Sequence 157, App
298	5	3.7	16	3	US-08-602-999A-313	Sequence 313, App	371	5	3.7	25	3	US-09-112-206-11	Sequence 11, Appl
299	5	3.7	16	4	US-09-500-124-313	Sequence 313, App	372	5	3.7	25	3	US-09-112-206-114	Sequence 114, App
300	5	3.7	16	4	US-09-712-368-9	Sequence 9, Appli	373	5	3.7	25	3	US-09-112-206-115	Sequence 115, App
301	5	3.7	17	2	US-08-637-759B-422	Sequence 422, App	374	5	3.7	25	3	US-09-112-206-157	Sequence 157, App
302	5	3.7	17	3	US-08-871-355A-422	Sequence 422, App	375	5	3.7	25	4	US-08-637-670-11	Sequence 11, Appl
303	5	3.7	17	3	US-09-201-945-422	Sequence 422, App	376	5	3.7	25	4	US-09-185-818-3	Sequence 3, Appli
304	5	3.7	17	4	US-08-634-137-6	Sequence 6, Appli	377	5	3.7	25	4	US-08-880-576-14	Sequence 14, Appl
305	5	3.7	18	1	US-08-499-523-15	Sequence 15, Appl	378	5	3.7	25	4	US-09-576-824A-114	Sequence 114, App
306	5	3.7	18	2	US-08-528-129A-6	Sequence 6, Appli	379	5	3.7	25	4	US-09-680-497-11	Sequence 11, Appl
307	5	3.7	18	3	US-08-128-345-15	Sequence 15, Appl	380	5	3.7	25	4	US-09-680-497-114	Sequence 114, App
308	5	3.7	18	4	US-08-838-128B-47	Sequence 47, Appl	381	5	3.7	25	4	US-09-680-497-115	Sequence 115, App
309	5	3.7	18	4	US-09-214-679-9	Sequence 9, Appli	382	5	3.7	25	4	US-09-680-497-157	Sequence 157, App
310	5	3.7	19	3	US-08-385-442-50	Sequence 50, Appl	383	5	3.7	25	5	PCT-US94-08380-24	Sequence 24, Appl
311	5	3.7	20	1	US-08-218-025A-58	Sequence 58, Appl	384	5	3.7	25	5	PCT-US94-08380-33	Sequence 33, Appl
312	5	3.7	20	1	US-08-218-025A-59	Sequence 59, Appl	385	5	3.7	25	5	PCT-US94-08380-38	Sequence 38, Appl
313	5	3.7	20	1	US-08-279-906A-16	Sequence 16, Appl	386	5	3.7	26	1	US-08-305-862-1	Sequence 1, Appli
314	5	3.7	20	1	US-08-306-116A-17	Sequence 17, Appl	387	5	3.7	26	2	US-08-417-210A-119	Sequence 119, App
315	5	3.7	20	2	US-08-433-133-95	Sequence 95, Appl	388	5	3.7	26	2	US-08-417-210A-120	Sequence 120, App
316	5	3.7	20	2	US-08-433-133-96	Sequence 96, Appl	389	5	3.7	26	4	US-09-136-159A-119	Sequence 119, App
317	5	3.7	20	3	US-08-602-999A-121	Sequence 121, App	390	5	3.7	26	4	US-09-136-159A-120	Sequence 120, App
318	5	3.7	20	4	US-09-500-124-121	Sequence 121, App	391	5	3.7	26	4	US-09-576-824A-115	Sequence 115, App
319	5	3.7	20	4	US-09-525-269A-23	Sequence 23, Appl	392	5	3.7	26	5	PCT-US93-06751-122	Sequence 122, App

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394	5	3.7	27	4	US-09-269-703A-2	Sequence 2, Appli	467	5	3.7	58	3	US-09-164-186-8	Sequence 8, Appli
395	5	3.7	28	2	US-08-031-538-48	Sequence 48, Appli	468	5	3.7	59	4	US-09-418-710-38	Sequence 38, Appli
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397	5	3.7	29	2	US-08-453-745A-7	Sequence 7, Appli	470	5	3.7	59	4	US-09-270-767-45960	Sequence 45960, A
398	5	3.7	29	2	US-08-453-520B-7	Sequence 7, Appli	471	5	3.7	59	4	US-09-839-479-37	Sequence 37, Appli
399	5	3.7	29	4	US-09-902-540-12822	Sequence 12822, A	472	5	3.7	59	4	US-09-839-479-49	Sequence 49, Appli
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401	5	3.7	30	3	US-09-135-166-29	Sequence 29, Appli	474	5	3.7	60	3	US-09-236-468A-11	Sequence 11, Appli
402	5	3.7	30	3	US-08-942-046-29	Sequence 29, Appli	475	5	3.7	60	4	US-09-328-352-4969	Sequence 4969, Ap
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408	5	3.7	34	4	US-09-205-258-323	Sequence 323, App	481	5	3.7	62	4	US-09-621-976-5475	Sequence 5475, Ap
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414	5	3.7	35	3	US-08-513-968-15	Sequence 15, Appli	487	5	3.7	63	4	US-09-248-796A-22562	Sequence 22562, A
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443	5	3.7	43	3	US-09-338-546-20	Sequence 20, Appli	516	5	3.7	69	4	US-09-195-457-9	Sequence 9, Appli
444	5	3.7	43	4	US-09-659-084-19	Sequence 19, Appli	517	5	3.7	69	4	US-09-489-039A-9115	Sequence 9115, Ap
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452	5	3.7	46	2	US-08-691-814B-47	Sequence 47, Appli	525	5	3.7	70	4	US-09-107-532A-6120	Sequence 6120, Ap
453	5	3.7	48	4	US-09-270-767-61956	Sequence 61956, A	526	5	3.7	70	4	US-09-134-000C-6148	Sequence 6148, Ap
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455	5	3.7	50	1	US-08-321-071A-31	Sequence 31, Appli	528	5	3.7	70	4	US-09-043-861-28	Sequence 28, Appli
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463	5	3.7	55	4	US-09-148-545-212	Sequence 212, App	536	5	3.7	72	1	US-08-482-111-13	Sequence 13, Appli
464	5	3.7	56	4	US-09-270-767-57759	Sequence 57759, A	537	5	3.7	72	4	US-09-107-532A-6178	Sequence 6178, Ap
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545	5	3.7	73	4	US-09-621-976-6443	Sequence 6443, Ap	618	5	3.7	89	1	US-08-303-275-190	Sequence 190, App
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551	5	3.7	74	4	US-09-270-767-53773	Sequence 53773, A	624	5	3.7	91	4	US-09-543-681A-4861	Sequence 4861, Ap
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556	5	3.7	75	4	US-09-952-768-66	Sequence 66, Appl	629	5	3.7	92	1	US-08-230-574-2	Sequence 2, Appl
557	5	3.7	76	4	US-09-540-236-3155	Sequence 3155, Ap	630	5	3.7	92	1	US-08-480-449-23	Sequence 23, Appl
558	5	3.7	76	4	US-09-270-767-61224	Sequence 61224, A	631	5	3.7	92	2	US-08-633-682-4	Sequence 4, Appl
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561	5	3.7	77	1	US-08-244-113-23	Sequence 23, Appl	634	5	3.7	92	2	US-08-535-116-3	Sequence 3, Appl
562	5	3.7	77	3	US-09-134-001C-3500	Sequence 3500, Ap	635	5	3.7	92	2	US-08-798-143-10	Sequence 10, Appl
563	5	3.7	77	4	US-09-255-518C-40	Sequence 40, Appl	636	5	3.7	92	2	US-08-467-123B-3	Sequence 3, Appl
564	5	3.7	77	4	US-09-270-767-39076	Sequence 39076, A	637	5	3.7	92	3	US-08-722-719-53	Sequence 53, Appl
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568	5	3.7	78	4	US-09-917-340-55	Sequence 55, Appl	641	5	3.7	92	3	US-09-133-521-7	Sequence 7, Appl
569	5	3.7	79	2	US-08-469-412A-12	Sequence 12, Appl	642	5	3.7	92	3	US-08-679-493A-161	Sequence 161, App
570	5	3.7	79	3	US-08-993-254-3	Sequence 3, Appl	643	5	3.7	92	3	US-08-479-603-23	Sequence 23, Appl
571	5	3.7	79	3	US-09-021-715-12	Sequence 12, Appl	644	5	3.7	92	4	US-09-334-951-53	Sequence 53, Appl
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574	5	3.7	79	4	US-09-621-976-4746	Sequence 4746, Ap	647	5	3.7	92	4	US-08-939-107-23	Sequence 23, Appl
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576	5	3.7	80	1	US-08-137-800-41	Sequence 41, Appl	649	5	3.7	92	4	US-09-334-954A-53	Sequence 53, Appl
577	5	3.7	80	1	US-08-477-383-41	Sequence 41, Appl	650	5	3.7	92	4	US-09-834-795A-33	Sequence 33, Appl
578	5	3.7	80	1	US-08-487-174-41	Sequence 41, Appl	651	5	3.7	92	4	US-09-467-638-9	Sequence 9, Appl
579	5	3.7	80	1	US-08-480-750-41	Sequence 41, Appl	652	5	3.7	92	4	US-09-067-447B-23	Sequence 23, Appl
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581	5	3.7	80	2	US-08-462-498-15	Sequence 15, Appl	654	5	3.7	92	4	US-09-571-013-55	Sequence 55, Appl
582	5	3.7	80	3	US-08-554-385-14	Sequence 14, Appl	655	5	3.7	92	6	5171841-1	Patent No. 5171841
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591	5	3.7	81	2	US-08-807-200-4	Sequence 4, Appl	664	5	3.7	93	3	US-09-230-371A-23	Sequence 23, Appl
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593	5	3.7	81	4	US-09-107-532A-5379	Sequence 5379, Ap	666	5	3.7	93	4	US-09-266-965-117	Sequence 117, App
594	5	3.7	81	4	US-09-270-767-36042	Sequence 36042, A	667	5	3.7	93	4	US-09-151-450-2	Sequence 2, Appl
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858	5	3.7	120	5	PCT-US94-07762-14	Sequence 14, Appl	931	137	3	US-09-328-352-5960	Sequence 5960, Ap
859	5	3.7	120	5	PCT-US94-07799-14	Sequence 14, Appl	932	137	4	US-09-904-615-163	Sequence 163, App
860	5	3.7	121	3	US-09-134-001C-4506	Sequence 4506, Ap	933	137	4	US-09-270-767-37229	Sequence 37229, A
861	5	3.7	122	4	US-09-154-750A-82	Sequence 82, Appl	934	137	4	US-09-270-767-52446	Sequence 52446, A
862	5	3.7	122	4	US-09-248-796A-23882	Sequence 23882, A	935	137	4	US-09-134-000C-4376	Sequence 4376, Ap
863	5	3.7	122	4	US-09-513-999C-4741	Sequence 4741, Ap	936	138	4	US-09-621-976-4421	Sequence 4421, Ap
864	5	3.7	122	4	US-09-513-999C-7811	Sequence 7811, Ap	937	138	4	US-09-270-767-37570	Sequence 37570, A
865	5	3.7	122	4	US-09-943-016-9911	Sequence 9911, Ap	938	138	4	US-09-270-767-52787	Sequence 52787, A
866	5	3.7	122	4	US-09-943-016-9911	Sequence 9911, Ap	939	138	4	US-09-050-739-90	Sequence 90, Appl
867	5	3.7	123	4	US-09-949-016-11254	Sequence 11254, A	940	139	4	US-09-248-796A-19628	Sequence 19628, A
868	5	3.7	123	4	US-09-134-000C-4424	Sequence 4424, Ap	941	139	4	US-09-949-016-10005	Sequence 10005, A
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870	5	3.7	123	4	US-09-270-767-39670	Sequence 39670, A	943	140	3	US-09-085-761A-34	Sequence 34, Appl
871	5	3.7	123	4	US-09-270-767-51359	Sequence 51359, A	944	140	3	US-09-252-991A-3152	Sequence 3152, A
872	5	3.7	123	4	US-09-816-248-3	Sequence 3, Appl	945	140	3	US-09-621-976-4121	Sequence 4121, Ap
873	5	3.7	123	4	US-09-540-236-3076	Sequence 3076, Ap	946	140	3	US-09-252-991A-20212	Sequence 20212, A
874	5	3.7	124	4	US-09-252-991A-21177	Sequence 21177, A	947	141	4	US-09-252-991A-24426	Sequence 24426, A
875	5	3.7	124	4	US-09-540-236-3076	Sequence 3076, Ap	948	141	4	US-09-252-991A-26729	Sequence 26729, A
876	5	3.7	124	4	US-09-513-999C-5038	Sequence 5038, Ap	949	141	4	US-09-198-452A-1144	Sequence 1144, Ap
877	5	3.7	125	1	US-08-462-949-24	Sequence 24, Appl	950	141	4	US-09-107-532A-4026	Sequence 4026, Ap
878	5	3.7	125	1	US-08-023-764B-24	Sequence 24, Appl	951	141	4	US-09-134-000C-6477	Sequence 6477, Ap
879	5	3.7	125	1	US-09-615-192A-321	Sequence 321, App	952	141	4	US-09-270-767-57219	Sequence 57219, A
880	5	3.7	125	4	US-09-732-210-72	Sequence 72, Appl	953	141	4	US-09-270-767-61539	Sequence 61539, A
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884	5	3.7	126	4	US-09-252-991A-16596	Sequence 16596, A	957	142	4	US-09-621-976-5395	Sequence 5395, Ap
885	5	3.7	126	4	US-09-621-976-4120	Sequence 4120, Ap	958	142	4	US-09-621-976-6716	Sequence 6716, Ap
886	5	3.7	126	4	US-09-898-659-37	Sequence 37, Appl	959	142	4	US-09-540-236-2489	Sequence 2489, Ap
887	5	3.7	126	4	US-09-107-433-3836	Sequence 3836, Ap	960	142	4	US-09-583-110-3744	Sequence 3744, Ap
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889	5	3.7	127	4	US-09-489-039A-8547	Sequence 8547, Ap	962	142	4	US-09-252-991A-21044	Sequence 21044, A
890	5	3.7	127	4	US-09-270-767-32286	Sequence 32286, A	963	143	4	US-09-252-991A-32948	Sequence 32948, A
891	5	3.7	127	4	US-09-902-540-10294	Sequence 10294, A	964	143	4	US-09-270-767-37046	Sequence 37046, A
892	5	3.7	128	4	US-09-711-164-337	Sequence 337, App	965	143	4	US-09-270-767-38860	Sequence 38860, A
893	5	3.7	128	4	US-09-583-110-5238	Sequence 5238, Ap	966	143	4	US-09-270-767-52263	Sequence 52263, A
894	5	3.7	129	4	US-09-732-210-63	Sequence 63, Appl	967	143	4	US-09-270-767-54077	Sequence 54077, A
895	5	3.7	129	4	US-09-489-039A-8776	Sequence 8776, Ap	968	143	4	US-09-082-920-6	Sequence 6, Appl
896	5	3.7	129	4	US-10-029-180-90	Sequence 90, Appl	969	144	3	US-09-480-237A-16	Sequence 16, Appl
897	5	3.7	130	4	US-09-252-991A-23006	Sequence 23006, A	970	144	4	US-09-107-532A-4029	Sequence 4029, Ap
898	5	3.7	131	4	US-09-631-594-78	Sequence 78, Appl	971	144	4	US-09-543-681A-6998	Sequence 6998, Ap
899	5	3.7	132	4	US-09-107-532A-7283	Sequence 7283, Ap	972	144	4	US-09-621-976-5094	Sequence 5094, Ap
900	5	3.7	132	4	US-09-583-110-4251	Sequence 4251, Ap	973	144	4	US-09-270-767-48278	Sequence 48278, A
901	5	3.7	132	4	US-09-774-639-170	Sequence 170, App	974	144	4	US-09-248-796A-20083	Sequence 20083, A
902	5	3.7	133	1	US-08-346-611-2	Sequence 2, Appl	975	144	2	US-08-406-057-8	Sequence 8, Appl
903	5	3.7	133	2	US-08-794-494-2	Sequence 2, Appl	976	145	2		

977 5 3.7 145 3 US-08-946-329A-55 Sequence 55, Appl
978 5 3.7 145 3 US-08-946-329A-56 Sequence 56, Appl
979 5 3.7 145 3 US-09-030-613-9 Sequence 9, Appl
980 5 3.7 145 3 US-08-958-316-8 Sequence 8, Appl
981 5 3.7 145 3 US-09-451-905-9 Sequence 9, Appl
982 5 3.7 145 4 US-09-252-991A-19228 Sequence 19228, A
983 5 3.7 146 3 US-09-105-343A-6 Sequence 6, Appl
984 5 3.7 146 4 US-09-252-991A-20372 Sequence 20372, A
985 5 3.7 146 4 US-09-252-991A-26454 Sequence 26454, A
986 5 3.7 146 4 US-09-543-681A-5030 Sequence 5030, Ap
987 5 3.7 146 4 US-09-640-211A-680 Sequence 680, App
988 5 3.7 146 4 US-09-902-540-12616 Sequence 12616, A
989 5 3.7 147 2 US-08-824-405-12 Sequence 12, Appl
990 5 3.7 147 4 US-09-621-976-4802 Sequence 4802, Ap
991 5 3.7 147 4 US-09-270-767-32088 Sequence 32088, A
992 5 3.7 147 4 US-09-270-767-58356 Sequence 58356, A
993 5 3.7 147 4 US-09-248-796A-20089 Sequence 20089, A
994 5 3.7 147 4 US-09-809-665A-56 Sequence 56, Appl
995 5 3.7 148 4 US-09-732-210-328 Sequence 328, App
996 5 3.7 148 4 US-09-540-236-2105 Sequence 2105, Ap
997 5 3.7 148 4 US-09-640-211A-1139 Sequence 1139, Ap
998 5 3.7 150 4 US-09-732-210-329 Sequence 329, App
999 5 3.7 150 4 US-09-270-767-61388 Sequence 61388, A
1000 5 3.7 151 4 US-09-732-210-1353 Sequence 1353, Ap

ALIGNMENTS

RESULT 1
US-09-270-767-35069
; Sequence 35069, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35069
; LENGTH: 133
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-35069

Query Match 5.2%; Score 7; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FVLENFS 17
Db 21 FVLENFS 27

RESULT 2
US-09-270-767-50286
; Sequence 50286, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50286
; LENGTH: 133
; TYPE: PRT
; ORGANISM: *Drosophila melanogaster*
US-09-270-767-50286

Query Match 5.2%; Score 7; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 FVLENFS 17
Db 21 FVLENFS 27

RESULT 3
US-09-902-540-13575
; Sequence 13575, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13575
; LENGTH: 138
; TYPE: PRT
; ORGANISM: *Myxococcus xanthus*
US-09-902-540-13575

Query Match 5.2%; Score 7; DB 4; Length 138;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 AGLPETS 69
Db 27 AGLPETS 33

RESULT 4
US-09-134-001C-5194
; Sequence 5194, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GFC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 5194
; LENGTH: 145
; TYPE: PRT
; ORGANISM: *Staphylococcus epidermidis*
US-09-134-001C-5194

Query Match 5.2%; Score 7; DB 3; Length 145;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
Db 21 DSATFVL 27

RESULT 5

US-08-887-534A-80
; Sequence 80, Application US/08887534A
; Patent No. 6455323
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/887,534A
; FILING DATE:
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-887-534A-80

Query Match 5.2%; Score 7; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
| | | | |
Db 286 DSATFVL 292

RESULT 6
US-09-527-431-80
; Sequence 80, Application US/09527431
; Patent No. 6485899
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 106
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive/6300 Sears Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/527,431
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/887,534
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rin-Laures, Li-Hsien
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/33996
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: (312) 474-6600
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-527-431-80

Query Match 5.2%; Score 7; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
| | | | |
Db 286 DSATFVL 292

RESULT 7
US-09-446-861-80
; Sequence 80, Application US/09446861
; Patent No. 6740485
; GENERAL INFORMATION:
; APPLICANT: Holden, David W.
; TITLE OF INVENTION: ANTI-BACTERIAL METHODS AND MATERIALS
; NUMBER OF SEQUENCES: 127
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Li-Hsien Rin-Laures, M.D.
; STREET: 6300 Sears Tower 233 South Wacker Drive
; CITY: Chicago
; STATE: IL
; COUNTRY: United States of America
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/446,861
; FILING DATE: 22-Mar-2000
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Li-Hsien Rin-Laures, M.D.
; REGISTRATION NUMBER: 33,547
; REFERENCE/DOCKET NUMBER: 28341/6314.PCP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; INFORMATION FOR SEQ ID NO: 80:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 411 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 80:
US-09-446-861-80

Query Match 5.2%; Score 7; DB 4; Length 411;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
| | | | |

Db 286 DSATFVL 292

RESULT 8

US-09-252-991A-20793
; Sequence 20793, Application US/09252991A
; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 20793

; LENGTH: 548

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-20793

Query Match 5.2%; Score 7; DB 4; Length 548;

Best Local Similarity 100.0%; Pred. No. 77;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 QRADPV 26

Db 247 QRADPV 253

RESULT 9

US-09-932-678-2

; Sequence 2, Application US/09932678

; Patent No. 6825034

; GENERAL INFORMATION:

; APPLICANT: Reeder, Ronald H.

; APPLICANT: Moorefield, Beth

; APPLICANT: Greene, Elizabeth A.

; TITLE OF INVENTION: HUMAN RN3 AND COMPOSITIONS AND METHODS RELATING

; FILE REFERENCE: 14538A-005810US

; CURRENT APPLICATION NUMBER: US/09/932,678

; CURRENT FILING DATE: 2001-08-16

; PRIOR APPLICATION NUMBER: 60/225,893

; PRIOR FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 651

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-932-678-2

Query Match 5.2%; Score 7; DB 4; Length 651;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 122 PQNDTVI 128

Db 614 PQNDTVI 620

RESULT 10

US-09-902-540-16517

; Sequence 16517, Application US/09902540

; Patent No. 6833447

; GENERAL INFORMATION:

; APPLICANT: Goldman, Barry S.

; APPLICANT: Hinkle, Gregory J.

; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 16517
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-16517

Query Match 4.4%; Score 6; DB 4; Length 36;

Best Local Similarity 100.0%; Pred. No. 65;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 LSVFLE 60

Db 20 LSVFLE 25

RESULT 11

US-08-428-488-13

; Sequence 13, Application US/08428488

; Patent No. 5624894

; GENERAL INFORMATION:

; APPLICANT: BODOR, Nicholas S.

; TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

; TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM

; NUMBER OF SEQUENCES: 107

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Burns, Doane, Swecker & Mathis

; STREET: P. O. Box 1404

; CITY: Alexandria

; STATE: Virginia

; COUNTRY: United States

; ZIP: 22313-1404

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/428,488

; FILING DATE: 27-APR-1995

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Baumeister, Mary Katherine

; REGISTRATION NUMBER: 26,254

; REFERENCE/DOCKET NUMBER: 028724-087

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (703) 836-6620

; TELEFAX: (703) 836-2021

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 39 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 1

; OTHER INFORMATION: /note= "Position 1 = H-Ser."

; FEATURE:

; NAME/KEY: Modified-site

; LOCATION: 39

; OTHER INFORMATION: /note= "Position 39 = Phe-OH."

; FEATURE:

; NAME/KEY: Modified-site

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; LOCATION: 30
; OTHER INFORMATION: /note= "Position 30 = Glu-NH2."
US-08-428-488-13

Query Match          4.4%; Score 6; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 70;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 KVPDGG 46
Db 21 KVPDGG 26

RESULT 12
US-08-960-022-12
; Sequence 12, Application US/08960022
; Patent No. 5976837
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: Lavallee, Edward R.
; APPLICANT: Racie, Lisa A.
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Spaulding, Vikki
; APPLICANT: Agostino, Michael J.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES
; TITLE OF INVENTION: ENCODING THEM
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/960,022
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Sprunger, Suzanne A.
; REGISTRATION NUMBER: 41,323
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8284
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 41 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-960-022-12

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; Sequence 32, Application US/09096724B
; Patent No. 6548290
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; GENERAL INFORMATION:
; APPLICANT: McGarity, Thomas J.
; APPLICANT: Kroll, Kristen
; APPLICANT: Kirschner, Marc W.
; TITLE OF INVENTION: Geminin Gene and Protein
; FILE REFERENCE: 0725.1055-001
; CURRENT APPLICATION NUMBER: US/09/096,724B
; CURRENT FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/085,371
; PRIOR FILING DATE: 1998-05-13
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 52
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; ORGANISM: human
US-09-096-724B-32

Query Match          4.4%; Score 6; DB 4; Length 52;
Best Local Similarity 100.0%; Pred. No. 92;
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Qy 60 ELSAGL 65
Db 16 ELSAGL 21

RESULT 14
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; Sequence 4130, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
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; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIGNAL
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US-09-621-976-4130

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; Sequence 24792, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
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; PRIOR FILING DATE: 1998-08-13
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OM protein - protein search, using sw model

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254	6	4.4	186	15	US-10-372-876-341	Sequence 341, App	327	6	4.4	290	15	US-10-369-493-12659	Sequence 12659, A
255	6	4.4	187	15	US-10-282-122A-56504	Sequence 56504, A	328	6	4.4	292	16	US-10-437-963-130275	Sequence 130275,
256	6	4.4	187	16	US-10-767-701-40084	Sequence 40084, A	329	6	4.4	292	16	US-10-425-115-202737	Sequence 202737,
257	6	4.4	188	16	US-10-425-115-205993	Sequence 205993,	330	6	4.4	293	16	US-10-767-701-44064	Sequence 44064, A
258	6	4.4	189	15	US-10-424-599-148735	Sequence 148735,	331	6	4.4	294	16	US-10-437-963-141196	Sequence 141196,
259	6	4.4	189	15	US-10-276-774-2120	Sequence 2120, Ap	332	6	4.4	294	17	US-10-732-923-20178	Sequence 20178, A
260	6	4.4	189	16	US-10-425-115-205277	Sequence 205277,	333	6	4.4	295	15	US-10-289-762-1123	Sequence 1123, Ap
261	6	4.4	193	15	US-10-264-237-2190	Sequence 2190, Ap	334	6	4.4	295	15	US-10-425-114-40997	Sequence 40997, A
262	6	4.4	193	15	US-10-335-977-5167	Sequence 5167, Ap	335	6	4.4	296	14	US-10-287-274-327	Sequence 327, App
263	6	4.4	195	15	US-10-424-599-173417	Sequence 173417	336	6	4.4	297	9	US-09-815-242-5149	Sequence 5149, Ap
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268	6	4.4	205	15	US-10-424-599-273598	Sequence 273598,	341	6	4.4	305	14	US-10-267-989-37	Sequence 37, Appl
269	6	4.4	209	14	US-10-178-055-2	Sequence 2, Appli	342	6	4.4	305	16	US-10-482-793-21	Sequence 21, Appl
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293	6	4.4	232	15	US-10-282-122A-67975	Sequence 67975, A	366	6	4.4	326	15	US-10-384-976-22	Sequence 22, Appl
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381	6	4.4	342	15	US-10-424-599-159871	Sequence 159871, A	454	6	4.4	420	17	US-10-735-256-2	Sequence 2, Appli
382	6	4.4	343	15	US-10-282-122A-60799	Sequence 60799, A	455	6	4.4	420	17	US-10-369-493-3861	Sequence 3861, Ap
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391	6	4.4	349	17	US-10-857-244-1	Sequence 1, Appli	464	6	4.4	434	15	US-10-282-122A-67746	Sequence 67746, A
392	6	4.4	351	15	US-10-282-122A-46888	Sequence 46888, A	465	6	4.4	436	15	US-10-425-114-69760	Sequence 69760, A
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394	6	4.4	360	15	US-10-424-599-277493	Sequence 277493, A	467	6	4.4	441	15	US-10-116-275-132	Sequence 132, App
395	6	4.4	362	9	US-09-767-870-10	Sequence 10, Appl	468	6	4.4	444	15	US-10-425-114-42253	Sequence 42253, A
396	6	4.4	362	14	US-10-242-568-10	Sequence 10, Appl	469	6	4.4	445	15	US-10-425-114-48747	Sequence 48747, A
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400	6	4.4	366	15	US-10-369-493-13763	Sequence 13763, A	473	6	4.4	451	15	US-10-369-493-9788	Sequence 9788, Ap
401	6	4.4	368	15	US-10-389-566-382	Sequence 382, App	474	6	4.4	451	16	US-10-425-115-199924	Sequence 199924, A
402	6	4.4	369	16	US-10-425-115-253705	Sequence 253705, A	475	6	4.4	452	14	US-10-238-075-504	Sequence 504, App
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410	6	4.4	384	9	US-09-853-918-20	Sequence 20, Appl	483	6	4.4	470	16	US-10-004-378A-103	Sequence 103, App
411	6	4.4	384	9	US-09-853-918-21	Sequence 21, Appl	484	6	4.4	470	16	US-10-437-963-172330	Sequence 172330, A
412	6	4.4	384	9	US-09-853-918-22	Sequence 22, Appl	485	6	4.4	473	17	US-10-732-923-9640	Sequence 9640, Ap
413	6	4.4	384	9	US-09-853-918-23	Sequence 23, Appl	486	6	4.4	474	15	US-10-425-114-62699	Sequence 62699, A
414	6	4.4	384	9	US-09-853-918-24	Sequence 24, Appl	487	6	4.4	474	15	US-10-425-114-63550	Sequence 63550, A
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416	6	4.4	384	9	US-09-853-918-26	Sequence 26, Appl	489	6	4.4	476	15	US-10-282-122A-73039	Sequence 73039, A
417	6	4.4	384	9	US-09-853-918-27	Sequence 27, Appl	490	6	4.4	477	15	US-10-282-122A-64300	Sequence 64300, A
418	6	4.4	384	9	US-09-853-918-28	Sequence 28, Appl	491	6	4.4	477	9	US-09-738-626-6986	Sequence 6986, Ap
419	6	4.4	384	9	US-09-853-918-29	Sequence 29, Appl	492	6	4.4	481	16	US-10-432-93A-29	Sequence 29, Appl
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423	6	4.4	385	9	US-09-853-918-32	Sequence 32, Appl	496	6	4.4	487	15	US-10-369-493-6111	Sequence 6111, Ap
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425	6	4.4	385	9	US-09-853-918-34	Sequence 34, Appl	498	6	4.4	487	15	US-10-755-889-44	Sequence 44, Appl
426	6	4.4	385	9	US-09-853-918-35	Sequence 35, Appl	499	6	4.4	490	9	US-09-741-669-455	Sequence 455, App
427	6	4.4	385	9	US-09-853-918-36	Sequence 36, Appl	500	6	4.4	491	9	US-09-815-242-10032	Sequence 10032, A
428	6	4.4	385	9	US-09-853-918-37	Sequence 37, Appl	501	6	4.4	491	9	US-09-815-242-14079	Sequence 14079, A
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432	6	4.4	390	10	US-09-972-546-8	Sequence 8, Appli	505	6	4.4	491	15	US-10-282-122A-75190	Sequence 75190, A
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438	6	4.4	395	15	US-10-424-599-261235	Sequence 261235, A	511	6	4.4	492	14	US-10-023-889-20	Sequence 20, Appl
439	6	4.4	398	16	US-10-424-599-261235	Sequence 8464, Ap	512	6	4.4	492	14	US-10-023-890-20	Sequence 20, Appl
440	6	4.4	399	15	US-10-282-122A-46839	Sequence 46839, A	513	6	4.4	492	14	US-10-024-197-20	Sequence 20, Appl
441	6	4.4	401	14	US-10-050-704-97	Sequence 97, Appl	514	6	4.4	492	14	US-10-023-894-20	Sequence 20, Appl
442	6	4.4	401	16	US-10-798-512-97	Sequence 97, Appl	515	6	4.4	492	17	US-10-306-686-19	Sequence 19, Appl
443	6	4.4	401	17	US-10-477-714-17	Sequence 17, Appl	516	6	4.4	492	17	US-10-901-216-20	Sequence 20, Appl
444	6	4.4	403	15	US-10-369-493-19185	Sequence 19185, A	517	6	4.4	492	17	US-10-494-672-72	Sequence 72, Appl
445	6	4.4	403	15	US-10-369-493-19334	Sequence 19334, A	518	6	4.4	492	17	US-10-657-280-19	Sequence 19, Appl
446	6	4.4	408	16	US-10-437-963-171710	Sequence 171710, A	519	6	4.4	493	15	US-10-335-977-5169	Sequence 5169, Ap
447	6	4.4	416	15	US-10-282-122A-46379	Sequence 46379, A	520	6	4.4	495	9	US-09-738-626-3801	Sequence 3801, Ap
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449	6	4.4	417	15	US-10-282-122A-64012	Sequence 64012, A	522	6	4.4	496	15	US-10-282-122A-64012	Sequence 64012, A

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525	6	4.4	512	15	US-10-369-493-14356	Sequence 14356, A	598	6	4.4	565	15	US-10-418-036-10	Sequence 10, Appl
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535	6	4.4	514	10	US-09-846-637A-10	Sequence 10, Appl	608	6	4.4	573	17	US-10-732-923-10708	Sequence 10708, A
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673	6	4.4	722	14	US-10-121-988-15	Sequence 15, Appl	746	6	4.4	888	14	US-10-121-050-544	Sequence 544, App
674	6	4.4	722	14	US-10-121-988-159	Sequence 159, App	747	6	4.4	888	14	US-10-141-755-544	Sequence 544, App
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676	6	4.4	722	14	US-10-200-562-159	Sequence 159, App	749	6	4.4	888	14	US-10-123-108-544	Sequence 544, App
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702	6	4.4	785	15	US-10-126-103-152	Sequence 152, App	775	6	4.4	888	14	US-10-147-500-544	Sequence 544, App
703	6	4.4	785	15	US-10-431-096-152	Sequence 152, App	776	6	4.4	888	14	US-10-147-503-544	Sequence 544, App
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724	6	4.4	888	13	US-10-036-342-35	Sequence 35, Appl	797	6	4.4	888	14	US-10-152-395-544	Sequence 544, App
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728	6	4.4	888	14	US-10-121-049-544	Sequence 544, App	801	6	4.4	888	14	US-10-127-837A-544	Sequence 544, App
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735	6	4.4	888	14	US-10-140-474-544	Sequence 544, App	808	6	4.4	888	14	US-10-127-850A-544	Sequence 544, App
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737	6	4.4	888	14	US-10-142-431-544	Sequence 544, App	810	6	4.4	888	14	US-10-128-684A-544	Sequence 544, App
738	6	4.4	888	14	US-10-143-114-544	Sequence 544, App	811	6	4.4	888	14	US-10-128-686A-544	Sequence 544, App
739	6	4.4	888	14	US-10-036-160-35	Sequence 35, Appl	812	6	4.4	888	14	US-10-128-690A-544	Sequence 544, App
740	6	4.4	888	14	US-10-142-419-544	Sequence 544, App	813	6	4.4	888	14	US-10-128-691A-544	Sequence 544, App
741	6	4.4	888	14			814	6	4.4	888	14		


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961 6 4.4 888 14 US-10-145-747-544 Sequence 544, App
962 6 4.4 888 14 US-10-145-752-544 Sequence 544, App
963 6 4.4 888 14 US-10-145-754-544 Sequence 544, App
964 6 4.4 888 14 US-10-145-755-544 Sequence 544, App
965 6 4.4 888 14 US-10-145-818-544 Sequence 544, App
966 6 4.4 888 14 US-10-145-820-544 Sequence 544, App
967 6 4.4 888 14 US-10-145-872-544 Sequence 544, App
968 6 4.4 888 14 US-10-145-873-544 Sequence 544, App
969 6 4.4 888 14 US-10-147-481-544 Sequence 544, App
970 6 4.4 888 14 US-10-147-482-544 Sequence 544, App
971 6 4.4 888 14 US-10-147-503-544 Sequence 544, App
972 6 4.4 888 14 US-10-147-522-544 Sequence 544, App
973 6 4.4 888 14 US-10-152-401-544 Sequence 544, App
974 6 4.4 888 14 US-10-157-783-544 Sequence 544, App
975 6 4.4 888 14 US-10-158-792-544 Sequence 544, App
976 6 4.4 888 14 US-10-158-462-544 Sequence 544, App
977 6 4.4 888 14 US-10-143-035-544 Sequence 544, App
978 6 4.4 888 14 US-10-145-751-544 Sequence 544, App
979 6 4.4 888 14 US-10-145-822-544 Sequence 544, App
980 6 4.4 888 14 US-10-145-824-544 Sequence 544, App
981 6 4.4 888 14 US-10-145-827-544 Sequence 544, App
982 6 4.4 888 14 US-10-145-869-544 Sequence 544, App
983 6 4.4 888 14 US-10-145-875-544 Sequence 544, App
984 6 4.4 888 14 US-10-145-877-544 Sequence 544, App
985 6 4.4 888 14 US-10-145-958-544 Sequence 544, App
986 6 4.4 888 14 US-10-146-787-544 Sequence 544, App
987 6 4.4 888 14 US-10-146-790-544 Sequence 544, App
988 6 4.4 888 14 US-10-146-793-544 Sequence 544, App
989 6 4.4 888 14 US-10-147-480-544 Sequence 544, App
990 6 4.4 888 14 US-10-147-485-544 Sequence 544, App
991 6 4.4 888 14 US-10-147-486-544 Sequence 544, App
992 6 4.4 888 14 US-10-147-487-544 Sequence 544, App
993 6 4.4 888 14 US-10-147-490-544 Sequence 544, App
994 6 4.4 888 14 US-10-147-494-544 Sequence 544, App
995 6 4.4 888 14 US-10-147-498-544 Sequence 544, App
996 6 4.4 888 14 US-10-147-514-544 Sequence 544, App
997 6 4.4 888 14 US-10-147-524-544 Sequence 544, App
998 6 4.4 888 14 US-10-152-379-544 Sequence 544, App
999 6 4.4 888 14 US-10-152-394-544 Sequence 544, App
1000 6 4.4 888 17 US-10-158-788-544 Sequence 544, App
```

ALIGNMENTS

```
RESULT 1
US-10-473-127-424
; Sequence 424, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 424
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-473-127-424
Query Match 100.0%; Score 135; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db 271 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 330
Qy 61 LSAGLPETSKYEVREVMVHQSNDPTKNIIREFASDFEVCWCYNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVREVMVHQSNDPTKNIIREFASDFEVCWCYNRFFRLDLLANEGYL 390
Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405
```

```
RESULT 2
US-10-473-127-429
; Sequence 429, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 429
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```
US-10-473-127-429
Query Match 100.0%; Score 135; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db 271 ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 330
Qy 61 LSAGLPETSKYEVREVMVHQSNDPTKNIIREFASDFEVCWCYNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVREVMVHQSNDPTKNIIREFASDFEVCWCYNRFFRLDLLANEGYL 390
Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405
```

```
RESULT 3
US-10-473-127-431
; Sequence 431, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
```

```
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 431
; LENGTH: 964
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-431

Query Match      100.0%; Score 135; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDPGNGVVRGYLSVFE 60
Db      271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDPGNGVVRGYLSVFE 330

Qy      61 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIREFASDFEVEGCGWGNRFRRLDLLANEGYL 120
Db      331 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIREFASDFEVEGCGWGNRFRRLDLLANEGYL 390

Qy      121 NPQNDTVILRFQVRS 135
Db      391 NPQNDTVILRFQVRS 405

RESULT 4
US-10-473-127-423
; Sequence 423, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 423
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-423

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDPGNGVVRGYLSVFE 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDPGNGVVRGYLSVFE 345

Qy      61 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIREFASDFEVEGCGWGNRFRRLDLLANEGYL 120
Db      346 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIREFASDFEVEGCGWGNRFRRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 5
US-10-473-127-425
; Sequence 425, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 425
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-425

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDPGNGVVRGYLSVFE 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDPGNGVVRGYLSVFE 345

Qy      61 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIREFASDFEVEGCGWGNRFRRLDLLANEGYL 120
Db      346 LSAGLPETSKYEYRVEVMVHQSCNDPTKNIIREFASDFEVEGCGWGNRFRRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 6
US-10-473-127-426
; Sequence 426, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026WO1
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
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; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 426
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-426

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 345

Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 7
US-10-473-127-427
; Sequence 427, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 427
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-427

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 345

Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420
```

```
Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 8
US-10-473-127-432
; Sequence 432, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
; PRIOR FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: 60/336,780
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/358,985
; PRIOR FILING DATE: 2002-02-20
; NUMBER OF SEQ ID NOS: 2041
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 432
; LENGTH: 979
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-473-127-432

Query Match      100.0%; Score 135; DB 16; Length 979;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 60
Db      286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGNVGVRGYLSVFL 345

Qy      61  LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 120
Db      346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIREFASDFEVCWCWYNRFFRLDLLANEGYL 405

Qy      121 NPQNDTVILRFQVRS 135
Db      406 NPQNDTVILRFQVRS 420

RESULT 9
US-10-473-127-430
; Sequence 430, Application US/10473127
; Publication No. US20040236091A1
; GENERAL INFORMATION:
; APPLICANT: Zycos Inc.
; TITLE OF INVENTION: TRANSLATIONAL PROFILING
; FILE REFERENCE: 08191-026W01
; CURRENT APPLICATION NUMBER: US/10/473,127
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/279,495
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: 60/292,544
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/310,801
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: 60/326,370
```

;; PRIOR FILING DATE: 2001-10-01
;; PRIOR APPLICATION NUMBER: 60/336,780
;; PRIOR FILING DATE: 2001-12-04
;; PRIOR APPLICATION NUMBER: 60/358,985
;; PRIOR FILING DATE: 2002-02-20
;; NUMBER OF SEQ ID NOS: 2041
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 430
;; LENGTH: 1016
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-473-127-430

Query Match 100.0%; Score 135; DB 16; Length 1016;
Best Local Similarity 100.0%; Pred. No. 1.4e-128;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 60
DB 323 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 382
QY 61 LSAGLPETSKYRYRVMVHQSCNDPTKNIREFASDFEVEGCGVNRFRRLDLLANEGYL 120
DB 383 LSAGLPETSKYRYRVMVHQSCNDPTKNIREFASDFEVEGCGVNRFRRLDLLANEGYL 442
QY 121 NPQDVTILRFQVRS 135
DB 443 NPQDVTILRFQVRS 457

RESULT 10
US-10-473-127-428
;; Sequence 428, Application US/10473127
;; Publication No. US20040236091A1
;; GENERAL INFORMATION:
;; APPLICANT: Zycos Inc.
;; TITLE OF INVENTION: TRANSLATIONAL PROFILING
;; FILE REFERENCE: 08191-026W01
;; CURRENT APPLICATION NUMBER: US/10/473,127
;; CURRENT FILING DATE: 2003-09-26
;; PRIOR APPLICATION NUMBER: 60/279,495
;; PRIOR FILING DATE: 2001-03-28
;; PRIOR APPLICATION NUMBER: 60/292,544
;; PRIOR FILING DATE: 2001-05-21
;; PRIOR APPLICATION NUMBER: 60/310,801
;; PRIOR FILING DATE: 2001-08-08
;; PRIOR APPLICATION NUMBER: 60/326,370
;; PRIOR FILING DATE: 2001-10-01
;; PRIOR APPLICATION NUMBER: 60/336,780
;; PRIOR FILING DATE: 2001-12-04
;; PRIOR APPLICATION NUMBER: 60/358,985
;; PRIOR FILING DATE: 2002-02-20
;; NUMBER OF SEQ ID NOS: 2041
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 428
;; LENGTH: 964
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-473-127-428

Query Match 67.4%; Score 91; DB 16; Length 964;
Best Local Similarity 100.0%; Pred. No. 1e-83;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 60
DB 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVVRGYLSVPLE 330
QY 61 LSAGLPETSKYRYRVMVHQSCNDPTKNIIR 91
DB 331 LSAGLPETSKYRYRVMVHQSCNDPTKNIIR 361

RESULT 11
US-09-992-238-33
;; Sequence 33, Application US/09992238
;; Publication No. US2003005444A1
;; GENERAL INFORMATION:
;; APPLICANT: BATTAGLINO, PETER
;; APPLICANT: FEDER, JOHN N
;; APPLICANT: MINTIER, GABE
;; APPLICANT: NELSON, THOMAS C
;; APPLICANT: RAMANATHAN, CHANDRA S
;; APPLICANT: WESTPHAL, RYAN
;; APPLICANT: CACACE, ANGELA
;; APPLICANT: BARBER, LAUREN
;; APPLICANT: HAWKEN, DONALD R
;; APPLICANT: KORNACKER, MICHAEL G
;; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY8,
;; TITLE OF INVENTION: EXPRESSED HIGHLY IN BRAIN
;; FILE REFERENCE: D0047NP
;; CURRENT APPLICATION NUMBER: US/09/992,238
;; CURRENT FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: 60/317166
;; PRIOR FILING DATE: 2001-09-04
;; PRIOR APPLICATION NUMBER: 60/308285
;; PRIOR FILING DATE: 2001-07-27
;; PRIOR APPLICATION NUMBER: 60/268581
;; PRIOR FILING DATE: 2001-02-14
;; PRIOR APPLICATION NUMBER: 60/248285
;; PRIOR FILING DATE: 2000-11-14
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: Patent in Ver. 2.1
;; SEQ ID NO 33
;; LENGTH: 55
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthesized
;; OTHER INFORMATION: peptide
US-09-992-238-33

Query Match 6.7%; Score 9; DB 10; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VPSYDSATF 11
DB 46 VPSYDSATF 54

RESULT 12
US-10-712-615-33
;; Sequence 33, Application US/10712615
;; Publication No. US20040214317A1
;; GENERAL INFORMATION:
;; APPLICANT: Bristol-Myers Squibb Company
;; TITLE OF INVENTION: A NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR, HGPRBMY8, EXPRESSED
;; TITLE OF INVENTION: HIGHLY IN BRAIN
;; FILE REFERENCE: D0047A-CIP
;; CURRENT APPLICATION NUMBER: US/10/712,615
;; CURRENT FILING DATE: 2003-11-13
;; PRIOR APPLICATION NUMBER: U.S. 09/992,238
;; PRIOR FILING DATE: 2001-11-14
;; PRIOR APPLICATION NUMBER: U.S. 60/248,285
;; PRIOR FILING DATE: 2000-11-14
;; PRIOR APPLICATION NUMBER: U.S. 60/268,581
;; PRIOR FILING DATE: 2001-02-14
;; PRIOR APPLICATION NUMBER: U.S. 60/308,285
;; PRIOR FILING DATE: 2001-07-27
;; PRIOR APPLICATION NUMBER: U.S. 60/317,166
;; PRIOR FILING DATE: 2001-09-04
;; NUMBER OF SEQ ID NOS: 134
;; SOFTWARE: Patent in version 3.2
;; SEQ ID NO 33
;; LENGTH: 55

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-712-615-33

Query Match          6.7%; Score 9; DB 16; Length 55;
Best Local Similarity 100.0%; Pred. No. 0.34;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      46 VPSYDSATF 54

RESULT 13
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; Sequence 115, Application US/09828644
; Patent No. US20020015998A1
; GENERAL INFORMATION:
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20020015998A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00196US1
; CURRENT APPLICATION NUMBER: US/09/828,644
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: 60/195,150
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,099
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,151
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,148
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,093
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/195,098
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: 60/230,149
; PRIOR FILING DATE: 2000-09-05
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 115
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-644-115

Query Match          6.7%; Score 9; DB 9; Length 242;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 VPSYDSATF 11
Db      172 VPSYDSATF 180

RESULT 14
US-09-841-741-2
; Sequence 2, Application US/09841741
; Publication No. US20030170779A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogeli, Gabriel
; TITLE OF INVENTION: No. US20030170779A1el G Protein-Coupled Receptors
; FILE REFERENCE: 00204.REGUS
; CURRENT APPLICATION NUMBER: US/09/841,741
; CURRENT FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: USSN 60/199,558
; PRIOR FILING DATE: 2000-04-25
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-841-741-2

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Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 VPSYDSATF 11
Db      389 VPSYDSATF 397

RESULT 15
US-10-345-332-5
; Sequence 5, Application US/10345332
; Publication No. US20030129705A1
; GENERAL INFORMATION:
; APPLICANT: Li et al.
; TITLE OF INVENTION: ISOLATED HUMAN G-PROTEIN COUPLED
; TITLE OF INVENTION: RECEPTORS, NUCLEIC ACID MOLECULES ENCODING HUMAN GPCR
; TITLE OF INVENTION: PROTEINS, AND USES THEREOF
; FILE REFERENCE: CLO00754CON
; CURRENT APPLICATION NUMBER: US/10/345,332
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 09/769,741
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/205,166
; PRIOR FILING DATE: 2000-05-18
; PRIOR APPLICATION NUMBER: 09/638,018
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 398
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-345-332-5

Query Match          6.7%; Score 9; DB 14; Length 398;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 VPSYDSATF 11
Db      389 VPSYDSATF 397

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GenCore version 5.1.6
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OM protein - protein search, using sw model

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558.211 Million cell updates/sec

Title: US-09-706-325-25

Perfect score: 135

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Post-processing: Listing first 1000 summaries

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6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	135	100.0	964	6	Abu03758 Human exp
7	135	100.0	979	3	Aab41571 Human ORF
8	135	100.0	979	4	Aae03660 Human TRA
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10	135	100.0	979	6	Abu03757 Human exp
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12	135	100.0	979	6	Abu03760 Human exp
13	135	100.0	979	6	Abu03761 Human exp
14	135	100.0	1016	4	Aam41047 Human pol
15	135	100.0	1016	6	Abu03764 Human exp
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19	9	6.7	242	5	Aau69568 Human G p
20	9	6.7	398	5	Abb81924 Human G-p
21	9	6.7	398	5	Aam51646 Human nGP
22	9	6.7	398	7	Abw01567 Human G-p
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24	9	6.7	485	5	Aae15642 Human G-p
25	9	6.7	485	7	Adc86473 Human GFC

26	9	6.7	485	7	ADD18025	Human G-p
27	9	6.7	508	4	AAB86428	Human bra
28	9	6.7	508	4	AAB61982	Human G-p
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52	9	6.7	508	8	ADO29034	Human nov
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56	5	5.9	179	6	ABU18596	Protein e
57	8	5.9	314	6	ABU19048	Protein e
58	7	5.2	145	5	ABP40349	Staphyloc
59	7	5.2	145	8	ADS04908	Staphyloc
60	7	5.2	147	5	ABP10945	Human ORF
61	7	5.2	198	6	ABU25828	Protein e
62	7	5.2	243	4	AAU41864	Human pol
63	7	5.2	244	4	ABG25183	Novel hum
64	7	5.2	285	4	ABG96337	Putative
65	7	5.2	357	4	AAG89758	C glutami
66	7	5.2	378	8	ADN25671	Bacterial
67	7	5.2	389	4	AAU50335	Propionib
68	7	5.2	389	6	ABW46854	Propionib
69	7	5.2	411	2	AAW97718	Staphyloc
70	7	5.2	419	4	ABG23515	Novel hum
71	7	5.2	441	4	ABB63022	Drosophil
72	7	5.2	507	5	ABB48420	Listeria
73	7	5.2	518	4	ABG04092	Novel hum
74	7	5.2	548	6	ABM72915	Staphyloc
75	7	5.2	548	7	ABO72047	Pseudomon
76	7	5.2	561	5	ABG97480	Human NOV
77	7	5.2	651	3	AAAB10936	Human RNA
78	7	5.2	651	5	ABH78308	Amino aci
79	7	5.2	806	6	ABM69133	Phototrab
80	6	4.4	14	5	ABG92758	A. nidula
81	6	4.4	21	7	ABO23430	Amino aci
82	6	4.4	21	8	ADR20818	Human sec
83	6	4.4	32	4	AAW88014	Human imm
84	6	4.4	32	7	ABO33898	Anti-GPI-
85	6	4.4	35	4	ABH37739	Peptide #
86	6	4.4	41	2	AAW80399	A secree
87	6	4.4	50	4	AAU13844	Human pol
88	6	4.4	50	4	AAU62083	Propionib
89	6	4.4	50	6	ABM58602	Propionib
90	6	4.4	51	4	AAU55773	Propionib
91	6	4.4	51	6	ABM52292	Propionib
92	6	4.4	52	4	AAU20569	Human sec
93	6	4.4	52	4	ABB15901	Human ner
94	6	4.4	57	5	ADK36443	Novel hum
95	6	4.4	58	3	AKG27550	Arabidops
96	6	4.4	59	4	AAO2813	Human pol
97	6	4.4	60	5	ABP05317	Human ORF
98	6	4.4	63	3	AAAB07696	A human 1

99	6	4.4	63	3	AB07605	Ab07605 A human i	172	6	4.4	141	3	AA03814	Human sec
100	6	4.4	63	7	AB32016	Ab32016 Human par	173	6	4.4	141	7	AB03428	Amino aci
101	6	4.4	63	8	AD13820	Ad13820 Human int	174	6	4.4	141	7	AD04482	Human pro
102	6	4.4	67	4	AU44848	Au44848 Propionib	175	6	4.4	141	8	AD02022	Human pro
103	6	4.4	67	6	ABM41367	Abm41367 Propionib	176	6	4.4	141	8	ADR20816	Human sec
104	6	4.4	68	2	AY12781	Aay12781 Human 5'	177	6	4.4	141	8	ABM81507	Tumour-as
105	6	4.4	69	6	ADA33640	Ad33640 Acinetoba	178	6	4.4	141	8	ADP55186	Human PRO
106	6	4.4	73	4	AA007952	Aa007952 Human pol	179	6	4.4	141	8	ADP24812	PRO polyp
107	6	4.4	74	4	AA005691	Aa005691 Human pol	180	6	4.4	141	8	ADP24812	PRO polyp
108	6	4.4	77	3	AG02196	Ag02196 Human sec	181	6	4.4	142	2	AA29012	T. gondii
109	6	4.4	79	7	AB065292	Ab065292 Klebsiell	182	6	4.4	142	4	AAU25483	T. gondii
110	6	4.4	80	2	AA36439	Aa36439 Fragment	183	6	4.4	142	7	ADG17074	T. gondii
111	6	4.4	80	3	AA41030	Aa41030 Zea mays	184	6	4.4	143	8	ADR09379	Human pro
112	6	4.4	80	4	ADM19701	Adm19701 Protein e	185	6	4.4	144	5	AB89243	Human pol
113	6	4.4	80	6	ADA11974	Ad11974 Human nov	186	6	4.4	145	3	AA06425	Arabidops
114	6	4.4	81	4	AU20343	Au20343 Human sec	187	6	4.4	145	6	AAU43782	Propionib
115	6	4.4	81	4	AAO12540	Aa012540 Human pol	188	6	4.4	145	6	ABM40301	Propionib
116	6	4.4	81	8	ADM94390	Adm94390 Corn MRP4	189	6	4.4	147	3	AAAB41086	Human ORF
117	6	4.4	88	3	ABA41970	Ab41970 Human ORF	190	6	4.4	147	4	AAU55797	Propionib
118	6	4.4	90	4	AAU50831	Au50831 Propionib	191	6	4.4	147	5	ABP34694	Human ORF
119	6	4.4	90	6	ABM47350	Abm47350 Propionib	192	6	4.4	147	6	ABM52316	Propionib
120	6	4.4	92	7	ADF60180	Adf60180 Human con	193	6	4.4	150	4	AAU93357	Human pol
121	6	4.4	94	4	AAU50268	Au50268 Propionib	194	6	4.4	150	4	AAU23508	Rat EST e
122	6	4.4	94	6	ABM46787	Abm46787 Propionib	195	6	4.4	150	6	ABO00769	Polypepti
123	6	4.4	96	3	AA54437	Aa54437 Zea mays	196	6	4.4	150	8	ADL30880	Human pro
124	6	4.4	96	4	AAO02838	Aa002838 Human pol	197	6	4.4	151	4	AAU22654	Human dig
125	6	4.4	97	5	ABP31142	Abp31142 Human per	198	6	4.4	151	4	AAU22648	Novel hum
126	6	4.4	98	3	AA41173	Aa41173 Zea mays	199	6	4.4	151	7	ADB32488	Human nov
127	6	4.4	98	4	AAU59025	Au59025 Propionib	200	6	4.4	154	4	AAU51799	Helicobac
128	6	4.4	98	6	ABM55544	Abm55544 Propionib	201	6	4.4	154	4	AAU25921	Human pro
129	6	4.4	99	4	AAU45195	Au45195 Propionib	202	6	4.4	157	4	AAU25818	Human pro
130	6	4.4	99	4	AAU20902	Au20902 Human nov	203	6	4.4	157	5	ABP29925	Streptoco
131	6	4.4	99	6	ABM41714	Abm41714 Propionib	204	6	4.4	157	5	ABP30763	Streptoco
132	6	4.4	99	6	ADA48310	Ad48310 Rice prot	205	6	4.4	158	4	AAU48532	Propionib
133	6	4.4	100	3	AA006687	Aa006687 Human sec	206	6	4.4	158	6	ABM45051	Propionib
134	6	4.4	102	6	ABU48490	Abu48490 Protein e	207	6	4.4	161	6	ABM69602	Phototrab
135	6	4.4	104	4	ABG18278	Abg18278 Novel hum	208	6	4.4	162	7	ADG73103	Pseudomon
136	6	4.4	105	4	AAO04294	Aa004294 Human pol	209	6	4.4	162	7	ADL12158	Pseudomon
137	6	4.4	107	3	AA012222	Aa012222 Zea mays	210	6	4.4	163	4	AAU47693	Propionib
138	6	4.4	109	4	AAO05925	Aa005925 Human pol	211	6	4.4	163	6	ABM44212	Propionib
139	6	4.4	112	3	AA000298	Aa000298 Human sec	212	6	4.4	166	4	AAU89205	Human sec
140	6	4.4	114	7	ABO33837	Ab033837 Human ant	213	6	4.4	166	6	ABP76311	Human GEN
141	6	4.4	114	7	ADM41860	Adm41860 Human ant	214	6	4.4	168	4	AAU31085	Novel hum
142	6	4.4	114	7	ADM41854	Adm41854 Human ant	215	6	4.4	168	5	ABP77410	Fungal me
143	6	4.4	114	7	ADM41857	Adm41857 Human ant	216	6	4.4	172	4	ADG27748	Human nov
144	6	4.4	116	3	AAAB41975	Aa41975 Human ORF	217	6	4.4	175	7	ADH87488	Enterococ
145	6	4.4	116	4	AAU40483	Au40483 Propionib	218	6	4.4	176	6	ABO00445	Novel hum
146	6	4.4	116	6	ABM37002	Abm37002 Propionib	219	6	4.4	177	6	ABU61919	Mouse gly
147	6	4.4	120	4	AAU50193	Au50193 Propionib	220	6	4.4	179	4	AAU18378	Human end
148	6	4.4	120	4	AAU32558	Au32558 Novel hum	221	6	4.4	180	5	ABG91061	Neisseria
149	6	4.4	120	6	ABM46712	Abm46712 Propionib	222	6	4.4	180	6	AAE32500	Human von
150	6	4.4	120	7	ADM41824	Adm41824 Human ant	223	6	4.4	181	4	AAU81496	S. epider
151	6	4.4	120	7	ADM41828	Adm41828 Human ant	224	6	4.4	181	6	ABP77694	N. gonorr
152	6	4.4	121	4	ABM60507	Abm60507 Drosophil	225	6	4.4	181	8	ADP08335	Neisseria
153	6	4.4	121	8	ADR86465	Adr86465 Aspergill	226	6	4.4	182	4	AAU39281	Human pol
154	6	4.4	124	7	ABE65333	Ab65333 Human pro	227	6	4.4	182	5	ABP38897	Staphyloc
155	6	4.4	126	3	AA411172	Aa411172 Zea mays	228	6	4.4	182	8	ADS05513	Staphyloc
156	6	4.4	126	4	ABG06291	Abg06291 Novel hum	229	6	4.4	183	6	ABU61914	Mouse gly
157	6	4.4	131	5	ABB48276	Abb48276 Listeria	230	6	4.4	183	6	ABU61913	Mouse gly
158	6	4.4	131	6	ABU32871	Abu32871 Protein e	231	6	4.4	183	6	ABU61918	Mouse gly
159	6	4.4	132	3	AA01510	Aa01510 Human sec	232	6	4.4	183	6	ABU61915	Mouse gly
160	6	4.4	132	3	AA01508	Aa01508 Human sec	233	6	4.4	183	6	ABU61916	Mouse gly
161	6	4.4	132	3	AA01509	Aa01509 Human sec	234	6	4.4	183	6	ABU61916	Mouse gly
162	6	4.4	132	4	AA089177	Aa089177 Human sec	235	6	4.4	184	6	ABP98153	Amino aci
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164	6	4.4	135	3	AA06426	Aa06426 Arabidops	237	6	4.4	185	3	AA58731	Breast an
165	6	4.4	135	5	ABP42709	Abp42709 Human ova	238	6	4.4	185	4	AAE03654	Human ext
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168	6	4.4	137	6	ABP75764	Abp75764 Human sec	241	6	4.4	187	6	ABU28580	Protein e
169	6	4.4	140	7	ABO67859	Ab067859 Pseudomon	242	6	4.4	188	3	AAAB41929	Human ORF
170	6	4.4	141	2	AAW55206	AaW55206 H. pylori	243	6	4.4	189	4	ABB11750	Human int
171	6	4.4	141	2	AAU01466	AaU01466 Polypepti	244	6	4.4	190	4	ABB65481	Drosophil

245	6	4.4	190	5	ABB07966	Abd07966 Human STU	318	6	4.4	274	6	ABU28813	Abu28813 Protein e
246	6	4.4	190	7	ADC10192	Adc10192 Human NOV	319	6	4.4	275	3	ABU24336	Abu24336 Arabidops
247	6	4.4	190	7	ADC10194	Adc10194 Human NOV	320	6	4.4	275	3	ABU63702	D. discoi
248	6	4.4	191	4	AM39280	Aam39280 Human pol	321	6	4.4	275	7	ADD15785	Dicyoste
249	6	4.4	191	8	AM84393	Aam84393 Human dia	322	6	4.4	275	7	ADD15785	Dicyoste
250	6	4.4	192	4	AM39279	Aam39279 Human pol	323	6	4.4	275	8	ADS26432	Bacterial
251	6	4.4	193	2	AAW55378	Aaw55378 H. pylori	324	6	4.4	276	8	ADS26801	Bacterial
252	6	4.4	193	5	ABB89814	Abb89814 Human pol	325	6	4.4	276	7	ABO69260	Pseudomon
253	6	4.4	193	5	AM50313	Aam50313 Helicobac	326	6	4.4	277	5	ABO62892	Klebsiell
254	6	4.4	193	7	ADJ73116	Adj73116 Human cel	327	6	4.4	277	5	ABP25427	Streptoco
255	6	4.4	193	8	ADJ75651	Adj75651 Marker ge	328	6	4.4	277	5	ABP25427	Streptoco
256	6	4.4	194	4	AAU62234	Aau62234 Propionib	329	6	4.4	278	4	ABG22062	Novel hum
257	6	4.4	194	6	ABM58753	Abm58753 Propionib	330	6	4.4	280	7	ADL22711	Human dis
258	6	4.4	196	7	ADC86647	Adc86647 Human GPC	331	6	4.4	284	7	ADG90654	Hepatic s
259	6	4.4	198	7	ABM74283	Abm74283 DNA clone	332	6	4.4	285	4	AAH88340	Human mem
260	6	4.4	200	6	AAO19812	Aao19812 Human gem	333	6	4.4	286	3	AAH88340	Human mem
261	6	4.4	203	3	AG06232	Aag06232 Human gem	334	6	4.4	287	5	ABH53974	Lactococc
262	6	4.4	206	3	RAY70007	Aay70007 Arabidops	335	6	4.4	289	4	AAU63895	Propionib
263	6	4.4	206	8	ADK16237	Adk16237 Nanoarcha	336	6	4.4	289	6	ABM60414	Propionib
264	6	4.4	207	3	AAH46926	Aah46926 Arabidops	337	6	4.4	290	8	ADS23626	Bacterial
265	6	4.4	208	6	ADA33459	Ada33459 Acinetoba	338	6	4.4	291	7	ABO80009	Pseudomon
266	6	4.4	209	3	AAH53928	Aay53928 Amino aci	339	6	4.4	292	3	AAH42102	Human pol
267	6	4.4	209	3	AB221031	Ab221031 Human nuc	340	6	4.4	292	4	AAH42102	Human pol
268	6	4.4	209	6	AB93776	Ab93776 Human pro	341	6	4.4	295	2	AAH35705	Chlamydia
269	6	4.4	209	6	AAO19811	Aao19811 Human gem	342	6	4.4	296	3	AAH18068	Arabidops
270	6	4.4	209	8	ADO20059	Ado20059 Human PRO	343	6	4.4	296	3	AAH18068	Amino aci
271	6	4.4	209	8	ADQ09242	Adq09242 Human LOC	344	6	4.4	296	4	AAH98857	E. coli g
272	6	4.4	209	8	ADP24931	Adp24931 PRO polyp	345	6	4.4	297	4	AAU33653	Pseudomon
273	6	4.4	210	4	AAH41065	Aam41065 Human pol	346	6	4.4	297	6	ABM70477	Photorhab
274	6	4.4	210	4	AAH41066	Aam41066 Human pol	347	6	4.4	297	6	ABU15572	Protein e
275	6	4.4	211	4	AAH41067	Aam41067 Human pol	348	6	4.4	299	3	AAH13995	Rape exte
276	6	4.4	211	3	AAH53929	Aay53929 Amino aci	349	6	4.4	300	4	ABH70965	Human ORF
277	6	4.4	211	8	ABM84391	Abm84391 Human dia	350	6	4.4	302	7	ABO80025	Drosophi
278	6	4.4	212	3	AAH46925	Aag46925 Arabidops	351	6	4.4	302	7	ABO80025	Pseudomon
279	6	4.4	215	4	AAH87344	Aab87344 Human gen	352	6	4.4	305	2	AAW53942	L.lactis
280	6	4.4	215	5	ABG65347	Abg65347 Human alb	353	6	4.4	305	2	AAW53945	L.lactis
281	6	4.4	215	6	ABR53611	AbR53611 Protein s	354	6	4.4	305	3	AAH18067	Arabidops
282	6	4.4	215	7	ADK64262	Adk64262 Disease t	355	6	4.4	305	8	ADQ60121	Murine-de
283	6	4.4	215	7	ABO69478	AbO69478 Pseudomon	356	6	4.4	306	2	AAH86912	Carrot ex
284	6	4.4	215	8	ADL78614	Adl78614 Albumin f	357	6	4.4	307	3	AAH28884	Arabidops
285	6	4.4	216	3	AAH46924	Aag46924 Arabidops	358	6	4.4	307	5	AAH50925	Yeast mit
286	6	4.4	216	8	ADG19768	Adg19768 G-protein	359	6	4.4	307	8	ADS44092	Bacterial
287	6	4.4	218	4	AAU46504	Aau46504 Propionib	360	6	4.4	310	5	AAE18733	Rice NADP
288	6	4.4	218	6	ABM43023	Abm43023 Propionib	361	6	4.4	311	7	ABO66123	Klebsiell
289	6	4.4	218	6	ADA22701	Ada22701 A. Gossyp	362	6	4.4	312	5	ABH49407	Listeria
290	6	4.4	219	3	AAH18069	Aag18069 Arabidops	363	6	4.4	313	2	AAH98419	H. pylori
291	6	4.4	222	4	AAH81517	Aag81517 S. epider	364	6	4.4	313	5	ABH49438	Listeria
292	6	4.4	225	7	ABO68718	AbO68718 Pseudomon	365	6	4.4	313	6	ABU32672	Protein e
293	6	4.4	226	4	AAH87424	Aab87424 Human gen	366	6	4.4	313	8	ADS28292	Bacterial
294	6	4.4	231	4	AAU30719	Aau30719 Novel hum	367	6	4.4	314	3	AAH30943	Arabidops
295	6	4.4	232	6	ABU40051	Abu40051 Protein e	368	6	4.4	315	4	AAH82503	S. epider
296	6	4.4	232	7	ABO81517	AbO81517 Pseudomon	369	6	4.4	315	5	ABH91295	Herbicida
297	6	4.4	233	6	ABU37916	AbU37916 Protein e	370	6	4.4	315	7	ABO83104	Pseudomon
298	6	4.4	234	8	ABM84392	Abm84392 Human dia	371	6	4.4	319	7	ADC95495	E. faeciu
299	6	4.4	235	3	AAH06231	Aag06231 Arabidops	372	6	4.4	321	8	ADH39735	Streptomy
300	6	4.4	241	3	AAH43660	Aab43660 Human can	373	6	4.4	321	4	ABG15289	Novel hum
301	6	4.4	241	6	ABU43943	Abu43943 Protein e	374	6	4.4	321	8	ADL04856	M. catarr
302	6	4.4	241	7	ABO69498	AbO69498 Pseudomon	375	6	4.4	324	5	ABP39235	Staphyloc
303	6	4.4	242	4	AAH87418	Aab87418 Human gen	376	6	4.4	324	8	ADG76328	Human Inc
304	6	4.4	244	7	ABO62700	AbO62700 Klebsiell	377	6	4.4	324	8	ADS05851	Staphyloc
305	6	4.4	245	3	AAH23927	Aag23927 Arabidops	378	6	4.4	325	4	AAH99830	AGC prote
306	6	4.4	248	8	ADS27183	AdS27183 Bacterial	379	6	4.4	325	5	ABU51227	Helicobac
307	6	4.4	250	7	ADC95110	Adc95110 E. faeciu	380	6	4.4	325	7	ADH86310	Enterococ
308	6	4.4	251	8	ADM06824	Adm06824 Environme	381	6	4.4	325	7	ABO83815	Pseudomon
309	6	4.4	253	3	AAH23926	Aag23926 Arabidops	382	6	4.4	325	8	ADJ38878	MSK2 amin
310	6	4.4	254	7	ADJ69376	Adj69376 Human hea	383	6	4.4	326	3	AAH77117	Ebola vir
311	6	4.4	256	3	AAH37115	Aay37115 Protein i	384	6	4.4	326	7	ADJ91992	Ebola vir
312	6	4.4	256	3	AAH58234	Aag58234 Arabidops	385	6	4.4	326	8	ADM48358	Zaire ebo
313	6	4.4	263	3	AAH38321	Abh38321 Human sec	386	6	4.4	326	8	ADM48348	Zaire ebo
314	6	4.4	263	6	ABU25968	Abu25968 Protein e	387	6	4.4	326	8	ADM48330	Zaire ebo
315	6	4.4	269	3	AAH45845	Aag45845 Arabidops	388	6	4.4	327	7	ABO63291	Klebsiell
316	6	4.4	269	4	ABH63951	Abh63951 Drosophi	389	6	4.4	328	3	AAH10914	Streptomy
317	6	4.4	270	3	AAH07532	Aag07532 Arabidops	390	6	4.4	328	3	AAH07547	Arabidops

391	6	4.4	329	7	ADP05714	Adf05714 Bacterial	464	6	4.4	384	5	AAE18166	Aae18166 Human mod
392	6	4.4	329	8	ADQ60123	Adq60123 His tag-T	465	6	4.4	384	5	AAE18173	Aae18173 Human mod
393	6	4.4	331	2	AAW63750	Aaw63750 A. nidula	466	6	4.4	384	5	AAE18170	Aae18170 Human mod
394	6	4.4	331	2	AAW76222	Aaw76222 Human che	467	6	4.4	384	5	AAE18171	Aae18171 Human mod
395	6	4.4	331	7	AAE39221	Aae39221 Barley NA	468	6	4.4	384	5	AAE18174	Aae18174 Human typ
396	6	4.4	331	7	ADO59263	Ado59263 Barley NA	469	6	4.4	384	5	AAE18167	Aae18167 Human typ
397	6	4.4	332	3	AB29250	Ab29250 Barley NA	470	6	4.4	385	5	AAE18181	Aae18181 Human typ
398	6	4.4	332	3	AB29250	Ab29250 Barley NA	471	6	4.4	385	5	AAE18179	Aae18179 Human mod
399	6	4.4	333	6	AB29250	Ab29250 Barley NA	472	6	4.4	385	5	AAE18182	Aae18182 Human mod
400	6	4.4	333	6	AB29250	Ab29250 Barley NA	473	6	4.4	385	5	AAE18184	Aae18184 Human mod
401	6	4.4	334	8	AB29250	Ab29250 Barley NA	474	6	4.4	385	5	AAE18180	Aae18180 Human mod
402	6	4.4	334	8	AB29250	Ab29250 Barley NA	475	6	4.4	385	5	AAE18177	Aae18177 Human mod
403	6	4.4	334	8	AB29250	Ab29250 Barley NA	476	6	4.4	385	5	AAE18178	Aae18178 Human mod
404	6	4.4	337	3	AB29250	Ab29250 Barley NA	477	6	4.4	385	5	AAE18183	Aae18183 Human typ
405	6	4.4	342	6	AB29250	Ab29250 Barley NA	478	6	4.4	385	5	AAE18176	Aae18176 Human mod
406	6	4.4	342	6	AB29250	Ab29250 Barley NA	479	6	4.4	385	7	ADH86508	Adh86508 Enterococ
407	6	4.4	342	6	AB29250	Ab29250 Barley NA	480	6	4.4	388	8	ADN23687	Adn23687 Bacterial
408	6	4.4	343	5	AB29250	Ab29250 Barley NA	481	6	4.4	390	4	AAU53476	Aau53476 Propionib
409	6	4.4	343	6	AB29250	Ab29250 Barley NA	482	6	4.4	390	5	AAO21482	Aao21482 Mature hu
410	6	4.4	343	6	AB29250	Ab29250 Barley NA	483	6	4.4	390	6	ABM49995	Abm49995 Propionib
411	6	4.4	344	8	AB29250	Ab29250 Barley NA	484	6	4.4	390	7	ADF28529	Adf28529 NGRHy mat
412	6	4.4	344	6	AB29250	Ab29250 Barley NA	485	6	4.4	390	8	ADS30198	Ads30198 Bacterial
413	6	4.4	345	6	AB29250	Ab29250 Barley NA	486	6	4.4	390	8	ADN2787	Adn2787 Bacterial
414	6	4.4	345	7	AB29250	Ab29250 Barley NA	487	6	4.4	394	8	ADS28248	Ads28248 Bacterial
415	6	4.4	345	8	AB29250	Ab29250 Barley NA	488	6	4.4	395	2	AA77086	Aar77086 Human sul
416	6	4.4	346	2	AAW82556	Aaw82556 Corn glyc	489	6	4.4	395	8	ADS24690	Ads24690 Bacterial
417	6	4.4	346	4	AAE05237	Aae05237 Corn glyc	490	6	4.4	397	2	AAW72086	Aaw72086 HSN-2 str
418	6	4.4	346	5	AAU76195	Aau76195 Corn glyc	491	6	4.4	397	4	ABG08517	Abg08517 Novel hum
419	6	4.4	346	7	AAE38775	Aae38775 Corn glyc	492	6	4.4	399	3	AA28983	Aag28983 Arabidops
420	6	4.4	347	7	ABO68187	Ab068187 Pseudomon	493	6	4.4	399	6	ABU18915	Abu18915 Protein e
421	6	4.4	350	3	AA47994	Aag47994 Arabidops	494	6	4.4	400	8	ADN47904	Adn47904 Thermococ
422	6	4.4	350	3	AA47994	Aag47994 Arabidops	495	6	4.4	401	6	AAE33486	Aae33486 Human REM
423	6	4.4	350	3	AA47994	Aag47994 Arabidops	496	6	4.4	401	7	ADE07875	Ade07875 Novel pro
424	6	4.4	350	6	ABM67855	Abm67855 Phototab	497	6	4.4	402	4	ABM45686	Abm45686 Propionib
425	6	4.4	350	7	ADF04333	Adf04333 Bacterial	498	6	4.4	402	6	ABM42205	Abm42205 Propionib
426	6	4.4	350	7	ABO77322	Ab077322 Pseudomon	499	6	4.4	403	8	ADS30301	Ads30301 Bacterial
427	6	4.4	350	8	ADN74365	Adn74365 Thale cre	500	6	4.4	403	8	ADS30152	Ads30152 Bacterial
428	6	4.4	351	3	AA47994	Aag47994 Arabidops	501	6	4.4	404	7	ABO80978	Ab080978 Pseudomon
429	6	4.4	351	3	AA47994	Aag47994 Arabidops	502	6	4.4	406	4	AAU67781	Aau67781 Propionib
430	6	4.4	351	3	AA47994	Aag47994 Arabidops	503	6	4.4	406	6	ABM64300	Abm64300 Propionib
431	6	4.4	351	6	ABU18964	Abu18964 Protein e	504	6	4.4	407	7	ABO83677	Ab083677 Pseudomon
432	6	4.4	351	8	ADN74459	Adn74459 Thale cre	505	6	4.4	409	4	ABG20682	Abg20682 Novel hum
433	6	4.4	351	8	ADN73727	Adn73727 Thale cre	506	6	4.4	410	2	AA10693	Aar10693 Cephalosp
434	6	4.4	353	3	AA47994	Aag47994 Arabidops	507	6	4.4	411	7	ADE08665	Ade08665 Novel pro
435	6	4.4	354	3	AA47994	Aag47994 Arabidops	508	6	4.4	416	4	AAU57642	Aau57642 Propionib
436	6	4.4	354	3	AA47994	Aag47994 Arabidops	509	6	4.4	416	6	ABM54161	Abm54161 Propionib
437	6	4.4	356	3	AA47994	Aag47994 Arabidops	510	6	4.4	416	6	ABU18455	Abu18455 Protein e
438	6	4.4	356	4	AA47994	Aag47994 Arabidops	511	6	4.4	417	6	ABU26217	Abu26217 Protein e
439	6	4.4	356	4	AA47994	Aag47994 Arabidops	512	6	4.4	418	6	AAE32502	Aae32502 Human wil
440	6	4.4	357	4	AA47994	Aag47994 Arabidops	513	6	4.4	418	8	ADS28776	Ads28776 Bacterial
441	6	4.4	358	3	AA47994	Aag47994 Arabidops	514	6	4.4	419	8	ADM72131	Adm72131 Human NTR
442	6	4.4	358	4	AA47994	Aag47994 Arabidops	515	6	4.4	420	4	ABG13928	Abg13928 Novel hum
443	6	4.4	359	3	AA47994	Aag47994 Arabidops	516	6	4.4	420	5	AAO21477	Aao21477 Human NGR
444	6	4.4	359	5	AB29250	Ab29250 Barley NA	517	6	4.4	420	6	ABR55621	Ab55621 Amino aci
445	6	4.4	362	4	AA47994	Aag47994 Arabidops	518	6	4.4	420	7	ADF28510	Adf28510 NGRHy pre
446	6	4.4	362	8	AA47994	Aag47994 Arabidops	519	6	4.4	420	8	ADS10516	Ads10516 Human the
447	6	4.4	363	4	AA47994	Aag47994 Arabidops	520	6	4.4	422	7	ABO72825	Ab072825 Pseudomon
448	6	4.4	363	8	ADP12978	Adp12978 Protein e	521	6	4.4	425	4	ABG24730	Abg24730 Novel hum
449	6	4.4	363	8	ADP12978	Adp12978 Protein e	522	6	4.4	425	7	ABO84328	Ab084328 Pseudomon
450	6	4.4	365	8	ADP12978	Adp12978 Protein e	523	6	4.4	427	5	ABU52159	Abu52159 Helicobac
451	6	4.4	365	8	ADP12978	Adp12978 Protein e	524	6	4.4	427	7	ABO74603	Ab074603 Pseudomon
452	6	4.4	366	8	ADP12978	Adp12978 Protein e	525	6	4.4	427	8	ADN21208	Adn21208 Bacterial
453	6	4.4	368	8	ADP12978	Adp12978 Protein e	526	6	4.4	427	8	ADN27073	Adn27073 Bacterial
454	6	4.4	369	4	AAU45721	Aau45721 Propionib	527	6	4.4	428	4	ABG20060	Abg20060 Novel hum
455	6	4.4	369	6	ABM42240	Abm42240 Propionib	528	6	4.4	428	6	ABP58648	Abp58648 Human cen
456	6	4.4	372	8	ADS44776	Ads44776 Bacterial	529	6	4.4	428	6	ABU33541	Abu33541 Protein e
457	6	4.4	376	6	ABP79804	Abp79804 N. gonorr	530	6	4.4	428	7	ADB65163	Adb65163 Human pro
458	6	4.4	378	8	ADN97130	Adn97130 ASPA01 as	531	6	4.4	433	8	ADS24137	Ads24137 Bacterial
459	6	4.4	381	7	ABO81224	Ab081224 Pseudomon	532	6	4.4	433	8	ADS27995	Ads27995 Bacterial
460	6	4.4	384	5	AAE18168	Aae18168 Human mod	533	6	4.4	434	6	ABU27232	Abu27232 Protein e
461	6	4.4	384	5	AAE18172	Aae18172 Human typ	534	6	4.4	434	6	ABU26890	Abu26890 Protein e
462	6	4.4	384	5	AAE18169	Aae18169 Human mod	535	6	4.4	436	6	ABU39822	Abu39822 Protein e
463	6	4.4	384	5	AAE18165	Aae18165 Human typ	536	6	4.4	437	7	ABO61095	Ab061095 Klebsiell

537	6	4.4	439	4	AAB96637	Aab96637 Putative	610	6	4.4	495	4	AAG90047	Aag90047 C glutami
538	6	4.4	440	5	ABB48444	Abb48444 Listeria	611	6	4.4	495	7	ADC32891	Adc32891 Human nov
539	6	4.4	441	7	ADD47749	Add47749 Human pro	612	6	4.4	495	7	ADD13447	Add13447 C. glutam
540	6	4.4	441	7	ADD47743	Add47743 Rat Prote	613	6	4.4	496	6	ABU36088	Abu36088 Protein e
541	6	4.4	441	7	ADD48842	Add48842 Rat Prote	614	6	4.4	500	6	ABM68189	Abm68189 Photorhab
542	6	4.4	441	7	ADD47747	Add47747 Rat Prote	615	6	4.4	505	7	ABO68361	AbO68361 Pseudomon
543	6	4.4	441	7	ADD47745	Add47745 Human pro	616	6	4.4	506	4	ABB58248	AbB58248 Drosophil
544	6	4.4	441	7	ADD48844	Add48844 Human pro	617	6	4.4	506	4	ADC97612	AdC97612 E. faeciu
545	6	4.4	442	7	ABO77396	AbO77396 Pseudomon	618	6	4.4	508	8	ABO79146	AbO79146 Pseudomon
546	6	4.4	443	7	ADC00947	AdC00947 Enterohae	619	6	4.4	508	8	ADN46956	AdN46956 Thermococ
547	6	4.4	445	5	ABP69674	AbP69674 Human pol	620	6	4.4	508	8	ADN20419	AdN20419 Bacterial
548	6	4.4	445	8	ADH71106	AdH71106 Human pro	621	6	4.4	510	3	ARG40249	Arg40249 Arabidops
549	6	4.4	448	5	ABP66147	AbP66147 Bifidobac	622	6	4.4	510	3	ARG39697	Arg39697 Arabidops
550	6	4.4	449	7	ABO68923	AbO68923 Pseudomon	623	6	4.4	512	8	ADS25580	AdS25580 Bacterial
551	6	4.4	451	8	ADN27135	AdN27135 Bacterial	624	6	4.4	512	8	ADS25323	AdS25323 Bacterial
552	6	4.4	452	4	ABB52566	AbB52566 Escherich	625	6	4.4	512	8	ADS26018	AdS26018 Bacterial
553	6	4.4	453	8	AQD65122	Aqd65122 Novel hum	626	6	4.4	513	4	ABB65522	AbB65522 Drosophil
554	6	4.4	453	8	ADN21519	AdN21519 Bacterial	627	6	4.4	514	2	AAR05431	Aar05431 Chinese h
555	6	4.4	458	5	ABB5232	AbB5232 Lactococc	628	6	4.4	514	2	AAR05432	Aar05432 Human IMP
556	6	4.4	460	6	ADA33775	Ada33775 Actinetoba	629	6	4.4	514	4	AAB96143	Aab96143 Putative
557	6	4.4	461	6	ABP57637	AbP57637 S. muraya	630	6	4.4	514	5	AAU10695	Aau10695 Reference
558	6	4.4	461	8	ADS45016	AdS45016 Bacterial	631	6	4.4	514	5	AAE18189	Aae18189 Human wil
559	6	4.4	462	6	ABU33870	AbU33870 Protein e	632	6	4.4	514	5	AAE18186	Aae18186 Human wil
560	6	4.4	462	7	ABO69558	AbO69558 Pseudomon	633	6	4.4	514	7	ADG63316	AdG63316 Human IMP
561	6	4.4	463	7	ABO68529	AbO68529 Pseudomon	634	6	4.4	514	7	ADG63312	AdG63312 Human IMP
562	6	4.4	464	7	ABO79302	AbO79302 Pseudomon	635	6	4.4	514	7	ADG63340	AdG63340 Mouse IMP
563	6	4.4	464	7	ABO78813	AbO78813 Pseudomon	636	6	4.4	514	7	ADG63314	AdG63314 Human IMP
564	6	4.4	465	7	ABM85311	AbM85311 Human pro	637	6	4.4	514	7	ADG63320	AdG63320 Human IMP
565	6	4.4	468	4	ABM60870	AbM60870 Drosophil	638	6	4.4	514	7	ADG63318	AdG63318 Human IMP
566	6	4.4	470	4	AAG78185	Aag78185 Mouse MIT	639	6	4.4	514	7	ADG63349	AdG63349 Human IMP
567	6	4.4	470	7	ABM85310	AbM85310 Mouse pro	640	6	4.4	514	7	ADG63310	AdG63310 Human wil
568	6	4.4	473	3	AAV85171	Aav85171 Human MSK	641	6	4.4	514	7	ADG63338	AdG63338 Mouse wil
569	6	4.4	475	7	ADM04878	AdM04878 Human pro	642	6	4.4	514	7	ADJ68634	Adj68634 Human hea
570	6	4.4	476	6	ADU45115	AdU45115 Protein e	643	6	4.4	514	8	ADO19228	Ado19228 Human PRO
571	6	4.4	477	6	ABU36376	AbU36376 Protein e	644	6	4.4	514	8	ADP98886	AdP98886 C. albica
572	6	4.4	477	8	ADQ66179	AdQ66179 Novel hum	645	6	4.4	514	8	ADS88152	AdS88152 Human pro
573	6	4.4	481	2	AAR44220	Aar44220 Threonine	646	6	4.4	514	8	ADS25064	AdS25064 Bacterial
574	6	4.4	481	4	AAV79721	Aav79721 Corynebac	647	6	4.4	515	4	ABR61379	AbR61379 Human pho
575	6	4.4	481	4	AAV93232	Aav93232 C. glutami	648	6	4.4	515	7	ADD27826	AdD27826 Human pho
576	6	4.4	481	5	ABU04679	AbJ04679 Mycobacte	649	6	4.4	515	7	ABW01496	AbW01496 Human pho
577	6	4.4	484	7	ABO67205	AbO67205 Klebsiell	650	6	4.4	515	7	ABW01545	AbW01545 Human pho
578	6	4.4	486	5	ABB47843	Abb47843 Listeria	651	6	4.4	515	7	ADJ70434	Adj70434 Human hea
579	6	4.4	487	6	ABU40885	AbU40885 Protein e	652	6	4.4	516	8	ADR09691	AdR09691 Human pro
580	6	4.4	487	8	ADJ71965	Adj71965 Human PMM	653	6	4.4	516	7	ABO73134	AbO73134 Pseudomon
581	6	4.4	487	8	ADN23458	AdN23458 Bacterial	654	6	4.4	516	7	ABO80756	AbO80756 Pseudomon
582	6	4.4	488	7	ADF06666	AdF06666 Bacterial	655	6	4.4	517	3	ARG46195	Arg46195 Arabidops
583	6	4.4	489	3	ABG40251	AbG40251 Arabidops	656	6	4.4	518	2	AAW67616	Aaw67616 A. nidula
584	6	4.4	489	7	ABO69831	AbO69831 Pseudomon	657	6	4.4	519	7	ABO65074	AbO65074 Klebsiell
585	6	4.4	490	8	ADO20015	AdO20015 Human PRO	658	6	4.4	520	7	ABO83759	AbO83759 Pseudomon
586	6	4.4	490	8	ADR14043	Adr14043 Human NP-	659	6	4.4	523	7	ADK62490	AdK62490 Disease t
587	6	4.4	491	3	ARG40250	Aag40250 Arabidops	660	6	4.4	523	8	ADS43504	AdS43504 Bacterial
588	6	4.4	491	4	AAU38486	Aau38486 Salmonell	661	6	4.4	523	8	ADS22445	AdS22445 Bacterial
589	6	4.4	491	4	AAU34439	Aau34439 E. coli c	662	6	4.4	526	7	ABM85867	AbM85867 Human pro
590	6	4.4	491	4	AAV98407	Aag98407 Escherich	663	6	4.4	527	7	ABO68450	AbO68450 Pseudomon
591	6	4.4	491	6	ABU27754	AbU27754 Protein e	664	6	4.4	527	8	ADP99173	AdP99173 Human tra
592	6	4.4	491	6	ABU48098	AbU48098 Protein e	665	6	4.4	528	7	ABO71167	AbO71167 Pseudomon
593	6	4.4	491	6	ABU31655	AbU31655 Protein e	666	6	4.4	529	7	ADH88063	AdH88063 Enterococ
594	6	4.4	491	6	ABU50003	AbU50003 Protein e	667	6	4.4	529	8	ADN21539	AdN21539 Bacterial
595	6	4.4	491	6	ABU47266	AbU47266 Protein e	668	6	4.4	529	8	ADR66377	AdR66377 Human pro
596	6	4.4	491	6	ABU28492	AbU28492 Protein e	669	6	4.4	529	8	ADR66719	AdR66719 Human pro
597	6	4.4	491	7	ADL46386	Adl46386 UDP-N-ace	670	6	4.4	531	7	ABO73763	AbO73763 Pseudomon
598	6	4.4	491	7	ADL46388	Adl46388 UDP-N-ace	671	6	4.4	532	7	ABO70495	AbO70495 Pseudomon
599	6	4.4	492	4	ABR61385	AbR61385 Murine ph	672	6	4.4	533	8	ADS22745	AdS22745 Bacterial
600	6	4.4	492	6	ABM68866	AbM68866 Photorhab	673	6	4.4	534	7	ABO78554	AbO78554 Pseudomon
601	6	4.4	492	7	ADD27828	Add27828 Mouse pho	674	6	4.4	535	6	ABU15732	AbU15732 Protein e
602	6	4.4	492	7	ABW01497	AbW01497 Murine ph	675	6	4.4	535	6	AAO24109	Aao24109 M acetivo
603	6	4.4	492	7	ABW01546	AbW01546 Murine ph	676	6	4.4	536	4	ABG13708	AbG13708 Novel hum
604	6	4.4	492	7	ADL65715	AdL65715 C. glutam	677	6	4.4	536	7	ADB66953	AdB66953 E. coli K
605	6	4.4	492	7	ABO65763	AbO65763 Klebsiell	678	6	4.4	536	7	ADC31190	AdC31190 Human nov
606	6	4.4	493	2	AAW55517	Aaw55517 H. pylori	679	6	4.4	540	7	ADD25637	Add25637 Binding d
607	6	4.4	493	5	AAW50311	Aam50311 Helicobac	680	6	4.4	542	4	ABG13709	AbG13709 Novel hum
608	6	4.4	494	7	ADF05705	AdF05705 Bacterial	681	6	4.4	544	6	ABR53439	AbR53439 Protein s
609	6	4.4	495	1	APB81325	ApB81325 Threonine	682	6	4.4	544	7	ADK64646	AdK64646 Disease t

683 6 4.4 545 4 AAB65649 Aab65649 Novel pro 756
684 6 4.4 545 8 ADI29256 Adi29256 Human MAR 757
685 6 4.4 546 7 ADK65863 Adk65863 Extensin- 758
686 6 4.4 550 6 ABM68260 Abm68260 Phototab 759
687 6 4.4 550 8 ADM80085 Adm80085 Spiromyaci 760
688 6 4.4 550 8 ADN97601 Adn97601 S ambofac 761
689 6 4.4 551 6 ABU38501 Abu38501 Protein e 762
690 6 4.4 551 6 ABU41945 Abu41945 Protein e 763
691 6 4.4 551 8 ADS26035 Ads26035 Bacterial 764
692 6 4.4 552 6 ABR53246 Abr53246 Protein s 765
693 6 4.4 552 7 ADK63668 Adk63668 Disease t 766
694 6 4.4 553 4 AAE04897 Aae04897 Human tra 767
695 6 4.4 553 5 AAU99944 Aau99944 Human sul 768
696 6 4.4 553 7 ADE82896 Ade82896 Human sul 769
697 6 4.4 554 4 AAB47275 Aab47275 hOAT4, 8/ 770
698 6 4.4 554 6 ABU40202 Abu40202 Protein e 771
699 6 4.4 557 8 ADM80084 Adm80084 Spiromyaci 772
700 6 4.4 557 8 ADN97600 Adn97600 S ambofac 773
701 6 4.4 557 8 ADS25335 Ads25335 Bacterial 774
702 6 4.4 558 7 ADM05589 Adm05589 Human pro 775
703 6 4.4 559 2 AAW50909 Aaw50909 Alteromon 776
704 6 4.4 559 3 AAG29748 Aag29748 Arabidops 777
705 6 4.4 560 3 AAB42058 Aab42058 Human ORF 778
706 6 4.4 560 8 ADS25588 Ads25588 Bacterial 779
707 6 4.4 561 2 AAW98552 Aaw98552 H. pylori 780
708 6 4.4 561 4 ABG09019 Abg09019 Novel hum 781
709 6 4.4 562 2 AAY06429 Aay06429 Human mat 782
710 6 4.4 562 4 AAU33507 Aau33507 Enterococ 783
711 6 4.4 562 4 AAB85160 Aab85160 Matrix me 784
712 6 4.4 563 2 AAY06428 Aay06428 Human mat 785
713 6 4.4 563 4 AAB93328 Aab93328 Human pro 786
714 6 4.4 563 5 ABP69374 Abp69374 Human pol 787
715 6 4.4 565 5 AAE31063 Aae31063 Ehrlichia 788
716 6 4.4 565 6 AAO19624 Aao19624 Human nox 789
717 6 4.4 565 8 ADG62954 Adg62954 Nox5, 3/2 790
718 6 4.4 565 8 ADJ57251 Adj57251 Human NOX 791
719 6 4.4 568 8 ADS21843 Ads21843 Bacterial 792
720 6 4.4 572 4 AAU35140 Aau35140 Enterococ 793
721 6 4.4 572 6 ABU14582 Abul14582 Protein e 794
722 6 4.4 572 8 ADS43544 Ads43544 Bacterial 795
723 6 4.4 573 7 ADB80097 Adb80097 Mycobacte 796
724 6 4.4 577 6 ABU22594 Abu22594 Protein e 797
725 6 4.4 578 4 ABB59765 Abb59765 Drosophil 798
726 6 4.4 581 8 ADL05053 Adl05053 M. catarr 799
727 6 4.4 582 8 ADM80083 Adm80083 Spiromyaci 800
728 6 4.4 582 8 ADN97599 Adn97599 S ambofac 801
729 6 4.4 584 4 ABG21351 Abg21351 Novel hum 802
730 6 4.4 592 7 ABO69726 Abo69726 Pseudomon 803
731 6 4.4 592 8 ADN25834 Adn25834 Bacterial 804
732 6 4.4 595 4 ABG30102 Abg30102 Novel hum 805
733 6 4.4 599 7 ABO68504 Abo68504 Pseudomon 806
734 6 4.4 601 3 AAY90851 Aay90851 Castor be 807
735 6 4.4 601 7 ABO81843 Abo81843 Pseudomon 808
736 6 4.4 605 2 AAR03923 Aar03923 Bacillus 809
737 6 4.4 605 6 ABU34329 Abu34329 Protein e 810
738 6 4.4 605 8 ADJ49552 Adj49552 Oii-assoc 811
739 6 4.4 606 4 AAM39875 Aam39875 Human pol 812
740 6 4.4 607 8 ADS30440 Ads30440 Bacterial 813
741 6 4.4 608 8 ADN20934 Adn20934 Bacterial 814
742 6 4.4 610 5 ABG80347 Abg80347 Clostridi 815
743 6 4.4 611 6 ABU17571 Abu17571 Protein e 816
744 6 4.4 611 8 ADJ49585 Adj49585 Oii-assoc 817
745 6 4.4 612 4 ABB58181 Abb58181 Drosophil 818
746 6 4.4 612 7 ADF74755 Adf74755 Murine dn 819
747 6 4.4 612 7 ABO76981 Abo76981 Pseudomon 820
748 6 4.4 612 8 ADR10271 Adr10271 Human pro 821
749 6 4.4 613 4 AAB95548 Aab95548 Human pro 822
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751 6 4.4 614 7 ABO79884 Abo79884 Pseudomon 824
752 6 4.4 614 8 ADN23263 Adn23263 Bacterial 825
753 6 4.4 614 8 ADN23262 Adn23262 Bacterial 826
754 6 4.4 615 8 ADS27325 Ads27325 Bacterial 827
755 6 4.4 617 3 AAG46194 Aag46194 Arabidops 828

5 AAO21865 Aao21865 Isoprenoi 618
4 AAM41661 Aam41661 Human pol 619
8 ADN24795 Adn24795 Bacterial 623
8 ADN22036 Adn22036 Bacterial 623
6 ABJ25392 Abj25392 Aspergill 630
6 ABM65172 Abm65172 Propionib 636
6 ABB93928 Abb93928 Herbicida 637
6 ABUS0354 Abu50354 Protein e 638
6 ABB97389 Abb97389 Novel hum 639
6 AAE09481 Aae09481 Mouse int 640
6 AAEU16881 Aaeu16881 Protein e 642
7 ABO83358 Abo83358 Pseudomon 642
8 ADS26595 Ads26595 Bacterial 663
8 ADS26970 Ads26970 Bacterial 663
6 AAB67308 Aab67308 ABC trans 664
4 ADA35769 Ada35769 Acinetoba 664
6 ABU44138 Abu44138 Protein e 667
6 ABU20436 Abu20436 Protein e 671
7 ABO83116 Abo83116 Pseudomon 671
2 AAR69870 Aar69870 Oncorhinc 679
2 AAR69868 Aar69868 Oncorhinc 679
7 ADM25673 Adm25673 Hyperther 679
2 AAR69869 Aar69869 Oncorhinc 680
2 AAR69871 Aar69871 Oncorhinc 680
3 AAG46193 Aag46193 Arabidops 680
4 AAB85339 Aab85339 Human sem 686
7 ABO79251 Abog79251 Pseudomon 692
3 AAG29747 Aag29747 Arabidops 694
4 ADO61597 Ado61597 Transcrip 694
8 ADM05114 Adm05114 Human pro 695
2 AAW55698 Aaw55698 H. pylori 696
2 AAY17207 Aay17207 H. pylori 696
5 AAMS0309 Aam50309 Helicobac 696
5 AAM50310 Aam50310 Helicobac 696
5 ABG93041 Abg93041 S. cerevi 699
6 ABJ25992 Abj25992 Aspergill 699
8 ADN18777 Adn18777 Bacterial 699
3 AAY85169 Aay85169 Mitogen a 705
7 ABO73430 Abou73430 Pseudomon 705
6 ABU48763 Abu48763 Protein e 706
4 ADP30092 Adp30092 Human nov 708
7 ADC31663 Adc31663 Human sec 710
8 ADQ65698 Adq65698 Novel hum 710
3 AAY85170 Aay85170 MSK2 spli 711
8 ADS23614 Ads23614 Bacterial 713
7 ABO83169 Abo83169 Pseudomon 720
2 AAW72211 Aaw72211 HSV-2 str 721
5 AAE17810 Aae17810 Herpes si 722
7 ADG74943 Adg74943 Human her 722
7 ADG75163 Adg75163 Human her 722
8 ADJ77801 Adj77801 Herpes si 722
6 ABR53052 Abr53052 Protein s 726
7 ADK62916 Adk62916 Disease t 726
8 ABO79773 Abo79773 Pseudomon 726
7 ABM83597 Abm83597 Human dia 733
8 ADN19789 Adn19789 Bacterial 738
6 AAE33189 Aae33189 Human LfE 739
6 ABUG2391 Abug2391 Leucine z 739
7 ADC31806 Adc31806 Human nov 739
7 ADJ68968 Adj68968 Human hea 739
8 ADN19863 Adn19863 Bacterial 739
6 AAU34688 Aau34688 E. coli c 752
6 ABU15119 Abu15119 Protein e 752
4 ABB66427 Abb66427 Drosophil 757
7 ABO63491 Abo63491 Klebsiell 762
2 AAR70690 Aar70690 Mesquite 762
3 AAY85175 Aay85175 Mitogen a 772
8 ADQ15048 Adq15048 Human can 772
6 AAY96167 Aay96167 Schizosac 776
5 ABG70086 Abg70086 Human pre 784
5 ABP68598 Abp68598 Human pan 784

829	6	4.4	785	4	AAB94320	Human PRO	Aab94320	902	6	4.4	888	6	ADB26989	Human PRO
830	6	4.4	785	6	ABU69617	Human NF-	Abu69617	903	6	4.4	888	6	ADB31276	Human PRO
831	6	4.4	785	7	ADJ69241	Human hea	Adj69241	904	6	4.4	888	6	ADA61204	Homo sapi
832	6	4.4	788	8	ABM83596	Human dia	Abm83596	905	6	4.4	888	6	ADB24351	Human PRO
833	6	4.4	789	8	ADs43700	Bacterial	Ads43700	906	6	4.4	888	6	ADA96680	Human PRO
834	6	4.4	793	7	ADC03400	Rice flow	Adc03400	907	6	4.4	888	6	ADA81252	Human PRO
835	6	4.4	794	4	AMW79803	Human PRO	Amw79803	908	6	4.4	888	6	ADA96128	Human PRO
836	6	4.4	794	7	ADB70250	C. neofor	Adb70250	909	6	4.4	888	6	ADB26437	Human PRO
837	6	4.4	807	8	ADs42567	Bacterial	Adg42567	910	6	4.4	888	6	ADB21922	Novel hum
838	6	4.4	808	4	ABG15173	Novel hum	Abg15173	911	6	4.4	888	6	ADA77701	Human PRO
839	6	4.4	807	8	ADT72097	Amino aci	Adt72097	912	6	4.4	888	7	ADB18441	Human PRO
840	6	4.4	815	7	ADM05553	Human PRO	Adm05553	913	6	4.4	888	7	ADA87124	Human PRO
841	6	4.4	816	7	ADC03488	Rice flow	Adc03488	914	6	4.4	888	7	ABO25134	Human sec
842	6	4.4	822	7	ADP70257	C. neofor	Adp70257	915	6	4.4	888	7	ADA88227	Human PRO
843	6	4.4	832	5	ABP35689	Fungal ZB	Abp35689	916	6	4.4	888	7	ADA46615	Novel hum
844	6	4.4	832	8	ADN18887	Bacterial	Adn18887	917	6	4.4	888	7	ADB28645	Human PRO
845	6	4.4	835	4	AMW78819	Human PRO	Aam78819	918	6	4.4	888	7	ADB29197	Human PRO
846	6	4.4	837	8	ADs29553	Bacterial	Ads29553	919	6	4.4	888	7	ADA77149	Human PRO
847	6	4.4	842	1	AAP93712	Sequence	Aap93712	920	6	4.4	888	7	ADA88779	Human PRO
848	6	4.4	859	4	ABG15965	Novel hum	Abg15965	921	6	4.4	888	7	ADA97784	Human PRO
849	6	4.4	865	6	ADW29140	Protein e	Adw29140	922	6	4.4	888	7	ADB27541	Human PRO
850	6	4.4	888	2	AAW19857	Human sem	Aaw19857	923	6	4.4	888	7	ADB22474	Novel hum
851	6	4.4	888	3	AAI18916	A novel p	Aai18916	924	6	4.4	888	7	ADA67165	Human PRO
852	6	4.4	888	4	AAU12443	Human PRO	Aau12443	925	6	4.4	888	7	ADB23026	Human PRO
853	6	4.4	888	5	AB884950	Human PRO	Ab884950	926	6	4.4	888	7	ADB23799	Human PRO
854	6	4.4	888	5	AB995556	Human ang	Abu95556	927	6	4.4	888	7	ADA92521	Novel hum
855	6	4.4	888	6	ABU03538	Angiogene	Abu03538	928	6	4.4	888	7	ADB15584	Human PRO
856	6	4.4	888	6	ABO17887	Novel hum	Abu17887	929	6	4.4	888	7	ADB38836	Novel hum
857	6	4.4	888	6	ABU69110	Human PRO	Abu69110	930	6	4.4	888	7	ADB38284	Novel hum
858	6	4.4	888	6	ABU81141	Human PRO	Abu81141	931	6	4.4	888	7	ADB66756	Novel hum
859	6	4.4	888	6	ABO19426	Human PRO	Abu19426	932	6	4.4	888	7	ADB89836	Human PRO
860	6	4.4	888	6	ADU66841	Human PRO	Abu66841	933	6	4.4	888	7	ADB890568	Human PRO
861	6	4.4	888	6	ABU59922	Novel sec	Abu59922	934	6	4.4	888	7	ADB39669	Novel hum
862	6	4.4	888	6	ABU69087	Human PRO	Abu69087	935	6	4.4	888	7	ADB47292	Novel hum
863	6	4.4	888	6	ABO25112	Human sec	Abu25112	936	6	4.4	888	7	ADB86899	Human PRO
864	6	4.4	888	6	ABU67117	Human sec	Abu67117	937	6	4.4	888	7	ADB77504	Novel hum
865	6	4.4	888	6	ABU81551	Human sec	Abu81551	938	6	4.4	888	7	ADB34661	Human PRO
866	6	4.4	888	6	ADA46063	Novel hum	Ada46063	939	6	4.4	888	7	ADB35765	Human PRO
867	6	4.4	888	6	ADA76560	Novel hum	Ada76560	940	6	4.4	888	7	ADB34109	Human PRO
868	6	4.4	888	6	ADA76494	Human PRO	Ada76494	941	6	4.4	888	7	ADB35213	Human PRO
869	6	4.4	888	6	ADA19144	Human PRO	Ada19144	942	6	4.4	888	7	ADB36317	Human PRO
870	6	4.4	888	6	ADA61767	Homo sapi	Ada61767	943	6	4.4	888	7	ADB46712	Novel hum
871	6	4.4	888	6	ADB19552	Novel hum	Adb19552	944	6	4.4	888	7	AAE39104	Human PRO
872	6	4.4	888	6	ADB28093	Human PRO	Adb28093	945	6	4.4	888	7	AAE39041	Human PRO
873	6	4.4	888	6	ADA86572	Novel hum	Ada86572	946	6	4.4	888	7	ADC50585	Novel hum
874	6	4.4	888	6	ADB16136	Human PRO	Adb16136	947	6	4.4	888	7	ADC72132	Novel hum
875	6	4.4	888	6	ADA47922	Human PRO	Ada47922	948	6	4.4	888	7	ADC29791	Novel hum
876	6	4.4	888	6	ADA67717	Human PRO	Ada67717	949	6	4.4	888	7	ADC60111	Novel hum
877	6	4.4	888	6	ADB30724	Human PRO	Adb30724	950	6	4.4	888	7	ADC53118	Novel hum
878	6	4.4	888	6	ADA86020	Novel hum	Ada86020	951	6	4.4	888	7	ADC57472	Novel hum
879	6	4.4	888	6	ADA97232	Human PRO	Ada97232	952	6	4.4	888	7	ADC60663	Novel hum
880	6	4.4	888	6	ADA79536	Human PRO	Ada79536	953	6	4.4	888	7	ADC51138	Novel hum
881	6	4.4	888	6	ADA87675	Novel hum	Ada87675	954	6	4.4	888	7	ADC65665	Human PRO
882	6	4.4	888	6	ADB16877	Human PRO	Ada16877	955	6	4.4	888	7	ADC54763	Novel hum
883	6	4.4	888	6	ADA91969	Novel hum	Ada91969	956	6	4.4	888	7	ADC53724	Novel hum
884	6	4.4	888	6	ADB15032	Human PRO	Adb15032	957	6	4.4	888	7	ADC59247	Novel hum
885	6	4.4	888	6	ADB18993	Novel hum	Adb18993	958	6	4.4	888	7	ADC56125	Novel hum
886	6	4.4	888	6	ADA94208	Human PRO	Ada94208	959	6	4.4	888	7	ADC58695	Novel hum
887	6	4.4	888	6	ADB20104	Novel hum	Adb20104	960	6	4.4	888	7	ADD03369	Novel hum
888	6	4.4	888	6	ADB13416	Human PRO	Adb13416	961	6	4.4	888	7	ADC90361	Novel hum
889	6	4.4	888	6	ABO43420	Novel hum	Abo43420	962	6	4.4	888	7	ADC69780	Human PRO
890	6	4.4	888	6	ADA74670	Human PRO	Ada74670	963	6	4.4	888	7	ADC48669	Human PRO
891	6	4.4	888	6	ADB24903	Human PRO	Adb24903	964	6	4.4	888	7	ADD10198	Human PRO
892	6	4.4	888	6	ADA82427	Human PRO	Ada82427	965	6	4.4	888	7	ADD04773	Novel hum
893	6	4.4	888	6	ADA75390	Human PRO	Ada75390	966	6	4.4	888	7	ADC80729	Novel hum
894	6	4.4	888	6	ADA85468	Novel hum	Ada85468	967	6	4.4	888	7	ADD11236	Human PRO
895	6	4.4	888	6	ADA84916	Novel hum	Ada84916	968	6	4.4	888	7	ADC10557	Human sec
896	6	4.4	888	6	ADB30172	Human PRO	Adb30172	969	6	4.4	888	7	ADC48117	Human PRO
897	6	4.4	888	6	ADA80700	Human PRO	Ada80700	970	6	4.4	888	7	ADC80177	Novel hum
898	6	4.4	888	6	ADA75942	Human PRO	Ada75942	971	6	4.4	888	7	ADD11517	Human sec
899	6	4.4	888	6	ADA47167	Human PRO	Ada47167	972	6	4.4	888	7	ADD09646	Human PRO
900	6	4.4	888	6	ADB25463	Human PRO	Adb25463	973	6	4.4	888	7	ADD41359	Novel hum
901	6	4.4	888	6	ADA93639	Human PRO	Ada93639	974	6	4.4	888	7	ADD52498	Human PRO

975 6 4.4 888 7 ADD53238 Human PRO
976 6 4.4 888 7 ADD53790 Novel hum
977 6 4.4 888 7 ADD37310 Human sec
978 6 4.4 888 7 ADD51946 Human PRO
979 6 4.4 888 7 ADD02745 Human PRO
980 6 4.4 888 7 ADD02179 Human PRO
981 6 4.4 888 7 ADD54361 Human PRO
982 6 4.4 888 7 ADD92678 Human PRO
983 6 4.4 888 7 ADD91574 Human PRO
984 6 4.4 888 7 ADE04188 Human PRO
985 6 4.4 888 7 ADE32485 Novel hum
986 6 4.4 888 7 ADE22417 Human PRO
987 6 4.4 888 7 ADD79641 Human PRO
988 6 4.4 888 7 ADE42177 Human PRO
989 6 4.4 888 7 ADE17994 Human PRO
990 6 4.4 888 7 ADD92126 Human PRO
991 6 4.4 888 7 ADE33589 Human PRO
992 6 4.4 888 7 ADE34141 Novel hum
993 6 4.4 888 7 ADD80193 Human PRO
994 6 4.4 888 7 ADD93230 Human PRO
995 6 4.4 888 7 ADE19650 Human PRO
996 6 4.4 888 7 ADE19098 Human PRO
997 6 4.4 888 7 ADE43294 Human PRO
998 6 4.4 888 7 ADD96083 Human PRO
999 6 4.4 888 7 ADE22969 Human PRO
1000 6 4.4 888 7 ADD79087 Human PRO

ALIGNMENTS

RESULT 1
AAE03670
ID AAE03670 standard; protein; 135 AA.
XX
AC AAE03670;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human TRAF7 TRAF-protein binding domain (TPBD) protein #3.
XX
KW Human; therapy; tumour necrosis factor; TNF receptor-associated factor;
KW adenocarcinoma; autoimmune disease; TRAF-protein binding domain; TPBD;
KW allergy; cancer; allograft rejection; sepsis; glioma; carcinoma; sarcoma;
KW melanoma; hamartoma; leukaemia; lymphoma; neoplasia; bone marrow aplasia;
KW benign proliferative disease; restenosis; fibrosis; balloon angioplasty;
KW keratinocyte hyperplasia; benign prostatic hypertrophy; keloid;
KW inflammatory hyperplasia; stress response; cellular proliferation;
KW immunoglobulin class switching; Ig; apoptosis.
XX Homo sapiens.
XX WO200132696-A2.
XX PD 10-MAY-2001.
XX
XX 03-NOV-2000; 2000WO-US030533.
XX PF
XX 05-NOV-1999; 99US-00434784.
XX PR
XX (BURN-) BURNHAM INST.
XX PA
XX Zapata JM, Reed JC;
XX FI
XX WPI; 2001-381115/40.
XX DR
XX New TRAF-protein binding domain polypeptide, useful e.g. for treatment
XX PT and diagnosis of cancer or autoimmune diseases, also related nucleic acid
XX PT and modulators.
XX
XX Claim 4; Page 147; 156pp; English.
XX PS
XX The present sequence is human TRAF7 TRAF (tumour necrosis factor, TNF
XX CC

CC receptor-associated factor)-protein binding domain (TPBD). TPBDs and/or
CC anti-TPBD antibodies (Ab) are used to identify agents for treatment of
CC autoimmune diseases, inflammation, allergy, allograft rejection, sepsis,
CC cancers such as gliomas, carcinomas, adenocarcinomas, sarcomas,
CC melanomas, hamartomas, leukaemias and lymphomas, benign proliferative
CC diseases, benign prostatic hypertrophy, keratinocyte hyperplasia,
CC neoplasia, keloid, inflammatory hyperplasia, fibrosis, smooth muscle cell
CC proliferation in arteries following balloon angioplasty (restenosis),
CC bone marrow aplasia or generally any condition that involves abnormal
CC apoptosis, cellular proliferation, differentiation or stress responses or
CC immunoglobulin class switching in B cells. Agents (Ab or
CC oligonucleotides) that bind specifically to TPBD or its nucleic acid are
CC useful for diagnosis of the specified diseases, particularly for
CC diagnosis or prognosis of cancer or for monitoring therapy
XX
SQ Sequence 135 AA;

Query Match 100.0%; Score 135; DB 4; Length 135;
Best Local Similarity 100.0%; Pred. No. 3.6e-133;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVESYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNWVGRGYLSVFL 60
Db 1 ELVESYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNWVGRGYLSVFL 60

Qy 61 LSAGLPSTSKYEVYRVEMVHOSCNDDPTXNIIREFASDFEVCWCYNRFFRLDLLANEGYL 120
Db 61 LSAGLPSTSKYEVYRVEMVHOSCNDDPTXNIIREFASDFEVCWCYNRFFRLDLLANEGYL 120

Qy 121 NPQNDTVILRPQVRS 135
Db 121 NPQNDTVILRPQVRS 135

RESULT 2
AAE03663
ID AAE03663 standard; protein; 153 AA.
XX
AC AAE03663;
XX
DT 29-AUG-2001 (first entry)
XX
DE Human TRAF7 TRAF-protein binding domain (TPBD) protein #2.
XX
KW Human; therapy; tumour necrosis factor; TNF receptor-associated factor;
KW adenocarcinoma; autoimmune disease; TRAF-protein binding domain; TPBD;
KW allergy; cancer; allograft rejection; sepsis; glioma; carcinoma; sarcoma;
KW melanoma; hamartoma; leukaemia; lymphoma; neoplasia; bone marrow aplasia;
KW benign proliferative disease; restenosis; fibrosis; balloon angioplasty;
KW keratinocyte hyperplasia; benign prostatic hypertrophy; keloid;
KW inflammatory hyperplasia; stress response; cellular proliferation;
KW immunoglobulin class switching; Ig; apoptosis.
XX Homo sapiens.
XX OS
XX WO200132696-A2.
XX PN
XX PD 10-MAY-2001.
XX
XX 03-NOV-2000; 2000WO-US030533.
XX PF
XX 05-NOV-1999; 99US-00434784.
XX PR
XX (BURN-) BURNHAM INST.
XX PA
XX Zapata JM, Reed JC;
XX FI
XX WPI; 2001-381115/40.
XX DR
XX N-PSDB; AAD08071.
XX
XX New TRAF-protein binding domain polypeptide, useful e.g. for treatment
XX PT and diagnosis of cancer or autoimmune diseases, also related nucleic acid
XX PT and modulators.
XX

XX PS Claim 4; Page 133-134; 156pp; English.

XX CC The present sequence is human TRAF7 TRAF (tumour necrosis factor, TNF

CC receptor-associated factor)-protein binding domain (TPBD) protein. TPBDs

CC and/or anti-TPBD antibodies (Ab) are used to identify agents for

CC treatment of autoimmune diseases, inflammation, allergy, allograft

CC rejection, sepsis, cancers such as gliomas, carcinomas, adenocarcinomas,

CC sarcomas, melanomas, hamatomas, leukaemias and lymphomas, benign

CC proliferative diseases, benign prostatic hypertrophy, keratinocyte

CC hyperplasia, neoplasia, keloid, inflammatory hyperplasia, fibrosis,

CC smooth muscle cell proliferation in arteries following balloon

CC angioplasty (restenosis), bone marrow aplasia or generally any condition

CC that involves abnormal apoptosis, cellular proliferation, differentiation

CC or stress responses or immunoglobulin class switching in B cells. Agents

CC (Ab or oligonucleotides) that bind specifically to TPBD or its nucleic

CC acid are useful for diagnosis of the specified diseases, particularly for

CC diagnosis or prognosis of cancer or for monitoring therapy

XX SQ Sequence 153 AA;

Query Match 100.0%; Score 135; DB 4; Length 153;

Best Local Similarity 100.0%; Pred. No. 4e-133;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVRGYLSVPLE 60

Db 4 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVRGYLSVPLE 63

Qy 61 LSAGLPETSKYRYRVEVMVHQSCNDPTKNIITREFASDFEVCWCYNRFFRLDLLANEGYL 120

Db 64 LSAGLPETSKYRYRVEVMVHQSCNDPTKNIITREFASDFEVCWCYNRFFRLDLLANEGYL 123

Qy 121 NPQNDTVILRFQVRS 135

Db 124 NPQNDTVILRFQVRS 138

RESULT 3

AA039261

ID AA039261 standard; protein; 964 AA.

AC AA039261;

XX 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2406.

XX Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;

KW peripheral nervous system; neuropathy; central nervous system; CNS;

KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;

KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;

KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;

KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.

XX 26-DEC-2000; 2000WO-US034263.

PR 23-DEC-1999; 99US-00471275.

PR 21-JAN-2000; 2000US-00488725.

PR 25-APR-2000; 2000US-00552317.

PR 20-JUN-2000; 2000US-00598042.

PR 19-JUL-2000; 2000US-00620312.

PR 03-AUG-2000; 2000US-00653450.

PR 14-SEP-2000; 2000US-00662191.

PR 19-OCT-2000; 2000US-00693036.

PR 29-NOV-2000; 2000US-00727344.

XX

PA (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren P, Wang D;

PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;

PI Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.

DR N-PSDB; AAI58417.

XX Novel nucleic acids and polypeptides, useful for treating disorders such

PT as central nervous system injuries.

XX Example 4; SEQ ID NO 2406; 10078pp; English.

PS The invention relates to human nucleic acids (AAI57798-AAI61369) and the

XX encoded polypeptides (AAM38642-RAA42213) with nontropic.

CC immunosuppressant and cytostatic activity. The polynucleotides are useful

CC in gene therapy. A composition containing a polypeptide or polynucleotide

CC of the invention may be used to treat diseases of the peripheral nervous

CC system, such as peripheral nervous injuries, peripheral neuropathy and

CC localised neuropathies and central nervous system diseases, such as

CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic

CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the

CC utilisation of the activities such as: immune system suppression,

CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic

CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,

CC assays for receptor activity, arthritis and inflammation, leukaemias and

CC C.N.S disorders. Note: The sequence data for this patent did not form

CC part of the printed specification

XX SQ Sequence 964 AA;

Query Match 100.0%; Score 135; DB 4; Length 964;

Best Local Similarity 100.0%; Pred. No. 2.3e-132;

Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVRGYLSVPLE 60

Db 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVRGYLSVPLE 330

Qy 61 LSAGLPETSKYRYRVEVMVHQSCNDPTKNIITREFASDFEVCWCYNRFFRLDLLANEGYL 120

Db 331 LSAGLPETSKYRYRVEVMVHQSCNDPTKNIITREFASDFEVCWCYNRFFRLDLLANEGYL 390

Qy 121 NPQNDTVILRFQVRS 135

Db 391 NPQNDTVILRFQVRS 405

RESULT 4

ABU03763

ID ABU03763 standard; protein; 964 AA.

XX ABU03763;

XX 29-JAN-2003 (first entry)

DE Human expressed protein tag (EPT) #429.

XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;

KW protease; protease inhibitor; transporter; cytoskeletal protein;

KW receptor; transcription factor; cancer; MHC;

KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;

KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

XX Homo sapiens.

OS WO200278524-A2.

PN 10-OCT-2002.

XX 28-MAR-2002; 2002WO-US009671.

XX

DE Human expressed protein tag (EPT) #424.
XX Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
KW protease; protease inhibitor; transporter; cytoskeletal protein;
KW receptor; transcription factor; cancer; MHC;
KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX
XX Homo sapiens.
XX WO200278524-A2.
XX 10-OCT-2002.
XX 28-MAR-2002; 2002WO-US009671.
XX 28-MAR-2001; 2001US-0279495P.
XX 21-MAY-2001; 2001US-0292544P.
XX 08-AUG-2001; 2001US-0310801P.
XX 01-OCT-2001; 2001US-0326370P.
XX 04-DEC-2001; 2001US-0336780P.
XX 20-FEB-2002; 2002US-0358985P.
XX (ZYCO-) ZYCO INC.
XX Chicx RM, Tomlinson AJ, Urban RG;
XX WPT; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
PT cytoskeletal proteins, receptors or transcription factors), useful for
PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
PT leukemia.
XX
XX Example 2; SEQ ID NO 424; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
CC fragment of a kinase, phosphatase, protease, protease inhibitor,
CC transporter, cytoskeletal protein, receptor or transcription factor. The
CC polypeptide is useful as an immunogenic composition for eliciting in a
CC mammal an immunogenic response directed against any of the purified
CC polypeptide. The purified polypeptide, or the antibody that binds to this
CC polypeptide, is useful for treating cancer. The polypeptide is also
CC useful for identifying compounds that binds to a naturally processed
CC class I or class II MHC-binding polypeptide. The polypeptides and
CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX Sequence 964 AA;
Query Match 100.0%; Score 135; DB 6; Length 964;
Best Local Similarity 100.0%; Pred. No. 2.3e-132;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELVPSYDSTFVLENFSTRQADPVYSPPLQVSGLCWRLKVPDNGVWVRGYLSVFELE 60
Db 271 ELVPSYDSTFVLENFSTRQADPVYSPPLQVSGLCWRLKVPDNGVWVRGYLSVFELE 330
QY 61 LSAGLPETSKYRYVEMVHQSCNDPTKNIREFASDFVEGCGVNRFRLLDLIANEGL 120
Db 331 LSAGLPETSKYRYVEMVHQSCNDPTKNIREFASDFVEGCGVNRFRLLDLIANEGL 390
QY 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405

RESULT 7
AAB41571
ID AAB41571 standard; protein; 979 AA.
XX
AC AAB41571;
XX 08-FEB-2001 (first entry)
DT
XX
DE Human ORFX ORF1335 polypeptide sequence SEQ ID NO:2670.
XX
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
KW vulnary; antipsoriatic; antiparkinsonian; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
XX Homo sapiens.
XX OS
XX WO200058473-A2.
XX
XX 05-OCT-2000.
XX
XX 31-MAR-2000; 2000WO-US008621.
XX
XX 31-MAR-1999; 99US-0127607P.
XX 02-APR-1999; 99US-0127636P.
XX 05-APR-1999; 99US-0127728P.
XX 30-MAR-2000; 2000US-00540763.
XX
XX (CURA-) CURAGEN CORP.
XX
XX Shimkets RA, Leach M;
XX
XX WPT; 2000-602362/57.
XX N-PSDB; AAC75780.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease.
XX
XX Claim 11; Page 1914-1916; 5507pp; English.
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
XX which represent the human ORFX open reading frames 1 to 3161. The ORFX
XX sequences have activities such as: cytostatic; hepatotropic; vulnary;
XX antipsoriatic; antiparkinsonian; neuroprotective; osteopathic;
XX anticonvulsant; antiarthritic; immunosuppressant; immunostimulant;
XX cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive;
XX dermatological; immunosuppressive; antiinflammatory; antibacterial;
XX antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The
XX sequences can be used for determining the presence of or predisposition
XX to, or preventing or treating pathological conditions associated with an
XX ORFX-associated disorder. The nucleic acids can be used to express ORFX
XX proteins in gene therapy vectors. The proteins and nucleic acids may be
XX used to treat cancers, proliferative disorders, neurodegenerative
XX disorders, osteoarthritis, graft vs host disease, cardiovascular disease,
XX diabetes mellitus, hypertension, hypothyroidism, cholesterol ester
XX storage, systemic lupus erythematosus, severe combined immunodeficiency
XX (SCID), AIDS, viral, bacterial or fungal infection, malaria, autoimmune
XX disorders, asthma, allergies, aplastic anaemia, burns, wounds, bone and
XX cartilage damage, nocturnal haemoglobinuria, antiinflammatory disease; to
XX enhance coagulation; to inhibit thrombosis; and as a contraceptive
XX Sequence 979 AA;

XX	Query Match	100.0%;	Score 135;	DB 3;	Length 979;
PT	Best Local Similarity	100.0%;	Pred. No. 2.3e-132;		
PT	Matches 135;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
XX					
PS	Claim 57; Page 123-127;	156pp;	English.		
XX					
CC	The present sequence is human TRAF7 TRAF (tumour necrosis factor, TNF				
CC	receptor-associated factor)-protein binding domain (TPBD). TPBDs and/or				
CC	anti-TPBD antibodies (Ab) are used to identify agents for treatment of				
CC	autoimmune diseases, inflammation, allergy, allograft rejection, sepsis,				
CC	cancers such as gliomas, carcinomas, adenocarcinomas, sarcomas,				
CC	melanomas, hamartomas, leukaemias and lymphomas, benign proliferative				
CC	diseases, benign prostatic hypertrophy, keratinocyte hyperplasia,				
CC	neoplasia, keloid, inflammatory hyperplasia, fibrosis, smooth muscle cell				
CC	proliferation in arteries following balloon angioplasty (restenosis),				
CC	bone marrow aplasia or generally any condition that involves abnormal				
CC	apoptosis, cellular proliferation, differentiation or stress responses or				
CC	immunoglobulin class switching in B cells. Agents (Ab or				
CC	oligonucleotides) that bind specifically to TPBD or its nucleic acid are				
CC	useful for diagnosis of the specified diseases, particularly for				
CC	diagnosis or prognosis of cancer or for monitoring therapy				
XX					
SQ	Sequence 979 AA;				
	Query Match	100.0%;	Score 135;	DB 4;	Length 979;
	Best Local Similarity	100.0%;	Pred. No. 2.3e-132;		
	Matches 135;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPDNGVVRGYYSVFLFLE	60		
DB	286	ELVPSYDSATFVLENFSTLQRADPVYSPPLQVSGLCWRLKVPDNGVVRGYYSVFLFLE	345		
QY	61	LSAGLPETSKYEVYRVMVHQSCNDPTKNIIRFASDFEVGECWGNRFFRLDLLANEGYL	120		
DB	346	LSAGLPETSKYEVYRVMVHQSCNDPTKNIIRFASDFEVGECWGNRFFRLDLLANEGYL	405		
QY	121	NPQNDTVILRFQVRS	135		
DB	406	NPQNDTVILRFQVRS	420		
RESULT 9					
ABU03766					
ID	ABU03766 standard; protein; 979 AA.				
XX					
AC	ABU03766;				
XX					
DT	29-JAN-2003 (first entry)				
XX					
DE	Human expressed protein tag (EPT) #432.				
XX					
KW	Translational profiling; expressed protein tag; EPT; kinase; phosphatase;				
KW	protease; protease inhibitor; transporter; cytoskeletal protein;				
KW	receptor; transcription factor; cancer; MHC;				
KW	major histocompatibility complex; myeloma; colon cancer; gastric cancer;				
KW	adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.				
XX					
OS	Homo sapiens.				
XX					
PN	WO200278524-A2.				
XX					
PD	10-OCT-2002.				
XX					
XX	28-MAR-2002; 2002WO-US009671.				
PF					
PR	28-MAR-2001; 2001US-0279495P.				
PR	21-MAY-2001; 2001US-0292544P.				
PR	08-AUG-2001; 2001US-0310801P.				
PR	01-OCT-2001; 2001US-0326370P.				
PR	04-DEC-2001; 2001US-0336780P.				
PR	20-FEB-2002; 2002US-0358985P.				
XX					


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XX OS Homo sapiens.
XX PN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCOS INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX DR WPI; 2003-040607/03.
XX PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX PT cytoskeletal proteins, receptors or transcription factors), useful for
XX PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX PT leukemia.
XX PS Example 2; SEQ ID NO 425; 134pp; English.
XX CC The invention describes a purified polypeptide, which comprises a
XX CC fragment of a kinase, phosphatase, protease, protease inhibitor,
XX CC transporter, cytoskeletal protein, receptor or transcription factor. The
XX CC polypeptide is useful as an immunogenic composition for eliciting in a
XX CC mammal an immunogenic response directed against any of the purified
XX CC polypeptide. The purified polypeptide, or the antibody that binds to this
XX CC polypeptide, is useful for treating cancer. The polypeptide is also
XX CC useful for identifying compounds that binds to a naturally processed
XX CC class I or class II MHC-binding polypeptide. The polypeptides and
XX CC polynucleotides are particularly useful for treating or preventing
XX CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
XX CC lymphoma or leukaemia. These are also useful for screening agents for
XX CC treating the above mentioned diseases. This sequence represents an
XX CC expressed protein tag (EPT) isolated from human tissue for translational
XX CC profiling. Note: This sequence does not appear in the printed
XX CC specification but was obtained in electronic format directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 979 AA;
XX Query Match 100.0%; Score 135; DB 6; Length 979;
XX Best Local Similarity 100.0%; Pred. No. 2.3e-132;
XX Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSVFL 60
DB 286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSVFL 345
QY 61 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 120
DB 346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 405
QY 121 NPQNDTVILRFQVRS 135
DB 406 NPQNDTVILRFQVRS 420
RESULT 12
ABU03760
ID ABU03760 standard; protein; 979 AA.
XX AC ABU03760;
XX DT 29-JAN-2003 (first entry)
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Human expressed protein tag (EPT) #426.

Translational profiling; expressed protein tag; EPT; kinase; phosphatase; protease; protease inhibitor; transporter; cytoskeletal protein; receptor; transcription factor; cancer; MHC; major histocompatibility complex; myeloma; colon cancer; gastric cancer; adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.

Homo sapiens.

OS
XX
PN WO200278524-A2.
PD 10-OCT-2002.
PF 28-MAR-2002; 2002WO-US009671.
PR 28-MAR-2001; 2001US-0279495P.
PR 21-MAY-2001; 2001US-0292544P.
PR 08-AUG-2001; 2001US-0310801P.
PR 01-OCT-2001; 2001US-0326370P.
PR 04-DEC-2001; 2001US-0336780P.
PR 20-FEB-2002; 2002US-0358985P.
PA (ZYCO-) ZYCOS INC.
PI Chicx RM, Tomlinson AJ, Urban RG;
DR WPI; 2003-040607/03.
PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters, cytoskeletal proteins, receptors or transcription factors), useful for treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or leukemia.
PS Example 2; SEQ ID NO 426; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a fragment of a kinase, phosphatase, protease, protease inhibitor, transporter, cytoskeletal protein, receptor or transcription factor. The polypeptide is useful as an immunogenic composition for eliciting in a mammal an immunogenic response directed against any of the purified polypeptide. The purified polypeptide, or the antibody that binds to this polypeptide, is useful for treating cancer. The polypeptide is also useful for identifying compounds that binds to a naturally processed class I or class II MHC-binding polypeptide. The polypeptides and polynucleotides are particularly useful for treating or preventing myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma, lymphoma or leukaemia. These are also useful for screening agents for treating the above mentioned diseases. This sequence represents an expressed protein tag (EPT) isolated from human tissue for translational profiling. Note: This sequence does not appear in the printed specification but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
SQ Sequence 979 AA;
Query Match 100.0%; Score 135; DB 6; Length 979;
Best Local Similarity 100.0%; Pred. No. 2.3e-132;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSVFL 60
DB 286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGVRGYLSVFL 345
QY 61 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 120
DB 346 LSAGLPETSKYEVYRVMVHQSCNDPTKNIIRFASDFEVCWCYGNRFFRLDLLANEGYL 405
QY 121 NPQNDTVILRFQVRS 135
DB 406 NPQNDTVILRFQVRS 420
RESULT 12
ABU03760
ID ABU03760 standard; protein; 979 AA.
XX AC ABU03760;
XX DT 29-JAN-2003 (first entry)

61 LSAGLPETSKYEVVMVHQSCNDPTKNI IREFASDFEVCWGYNRRFRDLNLLANEGYL 120
 346 LSAGLPETSKYEVVMVHQSCNDPTKNI IREFASDFEVCWGYNRRFRDLNLLANEGYL 405
 QY 121 NPQNDTVILRFQVRS 135
 Db 406 NPQNDTVILRFQVRS 420
 RESULT 14
 AAM41047
 ID AAM41047 standard; protein; 1016 AA.
 XX
 AC AAM41047;
 XX
 DT 22-OCT-2001 (first entry)
 XX
 DE Human polypeptide SEQ ID NO 5978.
 KW Human; nontropic; immunosuppressant; cytostatic; gene therapy; cancer;
 KW peripheral nervous system; neuropathy; central nervous system; CNS;
 KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
 KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
 KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
 KW leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US034263.
 XX
 PR 23-DEC-1999; 99US-00471275.
 PR 21-JAN-2000; 2000US-00488725.
 PR 25-APR-2000; 2000US-00552317.
 PR 20-JUN-2000; 2000US-00598042.
 PR 19-JUL-2000; 2000US-00620312.
 PR 03-AUG-2000; 2000US-00653450.
 PR 14-SEP-2000; 2000US-00662191.
 PR 19-OCT-2000; 2000US-00693036.
 PR 29-NOV-2000; 2000US-00727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J, Zhao QA;
 PI Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI; 2001-442253/47.
 DR N-FSDB; AAI60203.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders such
 as central nervous system injuries.
 XX
 PS Example 2; SEQ ID NO 5978; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and the
 encoded polypeptides (AAM38642-AAM42213) with nontropic,
 immunosuppressant and cytostatic activity. The polynucleotides are useful
 in gene therapy. A composition containing a polypeptide or polynucleotide
 of the invention may be used to treat diseases of the peripheral nervous
 system, such as peripheral nervous injuries, peripheral neuropathy and
 localised neuropathies and central nervous system diseases, such as
 Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 utilisation of the activities such as: Immune system suppression,
 Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 assays for receptor activity, arthritis and inflammation, leukaemias and
 C.N.S disorders. Note: The sequence data for this patent did not form
 part of the printed specification

RESULT 13
 ABU03761
 ID ABU03761 standard; protein; 979 AA.
 XX
 AC ABU03761;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Human expressed protein tag (EPT) #427.
 XX
 KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 XX
 OS Homo sapiens.
 XX
 FN WO200278524-A2.
 XX
 PD 10-OCT-2002.
 XX
 PF 28-MAR-2002; 2002WO-US009671.
 XX
 PR 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX
 PA (ZYCO-) ZYCOS INC.
 XX
 PI Chicz RM, Tomlinson AJ, Urban RG;
 XX
 DR WPI; 2003-040607/03.
 XX
 PT New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 427; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (EPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 979 AA;
 Query Match 100.0%; Score 135; DB 6; Length 979;
 Best Local Similarity 100.0%; Pred. No. 2.3e-132;
 Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLRLKVPYDNGVVRGYLSVFLE 60
 Db 286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSLCWLRLKVPYDNGVVRGYLSVFLE 345

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XX SQ Sequence 1016 AA;
XX Query Match 100.0%; Score 135; DB 4; Length 1016;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-132;
XX Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGRGYLSVPLE 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
323 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGRGYLSVPLE 382
Qy 61 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIRFASDFEVEGECWGNRFFRLDLLANEGYL 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
383 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIRFASDFEVEGECWGNRFFRLDLLANEGYL 442
Qy 121 NPQNDTVILRFQVRS 135
Db ||||||||||||||||
443 NPQNDTVILRFQVRS 457

RESULT 15
ABU03764
ID ABU03764 standard; protein; 1016 AA.
XX AC ABU03764;
XX DT 29-JAN-2003 (first entry)
XX DE Human expressed protein tag (EPT) #430.
XX KW Translational profiling; expressed protein tag; EPT; kinase; phosphatase;
XX KW protease; protease inhibitor; transporter; cytoskeletal protein;
XX KW receptor; transcription factor; cancer; MHC;
XX KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
XX KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
XX OS Homo sapiens.
XX FN WO200278524-A2.
XX PD 10-OCT-2002.
XX PF 28-MAR-2002; 2002WO-US009671.
XX PR 28-MAR-2001; 2001US-0279495P.
XX PR 21-MAY-2001; 2001US-0292544P.
XX PR 08-AUG-2001; 2001US-0310801P.
XX PR 01-OCT-2001; 2001US-0326370P.
XX PR 04-DEC-2001; 2001US-0336780P.
XX PR 20-FEB-2002; 2002US-0358985P.
XX PA (ZYCO-) ZYCO INC.
XX PI Chicx RM, Tomlinson AJ, Urban RG;
XX WPI; 2003-040607/03.
XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
XX cytoskeletal proteins, receptors or transcription factors), useful for
XX treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
XX leukemia.
XX Example 2; SEQ ID NO 430; 134pp; English.
XX The invention describes a purified polypeptide, which comprises a
XX fragment of a kinase, phosphatase, protease, protease inhibitor,
XX transporter, cytoskeletal protein, receptor or transcription factor. The
XX polypeptide is useful as an immunogenic composition for eliciting in a
XX mammal an immunogenic response directed against any of the purified
XX polypeptide. The purified polypeptide, or the antibody that binds to this
XX polypeptide, is useful for treating cancer. The polypeptide is also
XX useful for identifying compounds that binds to a naturally processed
XX class I or class II MHC-binding polypeptide. The polypeptides and

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CC polynucleotides are particularly useful for treating or preventing
CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
CC lymphoma or leukaemia. These are also useful for screening agents for
CC treating the above mentioned diseases. This sequence represents an
CC expressed protein tag (EPT) isolated from human tissue for translational
CC profiling. Note: This sequence does not appear in the printed
CC specification but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 1016 AA;
XX Query Match 100.0%; Score 135; DB 6; Length 1016;
XX Best Local Similarity 100.0%; Pred. No. 2.4e-132;
XX Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGRGYLSVPLE 60
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
323 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGRGYLSVPLE 382
Qy 61 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIRFASDFEVEGECWGNRFFRLDLLANEGYL 120
Db ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
383 LSAGLPETSKYEXYRVMVHQSCNDPTKNIIRFASDFEVEGECWGNRFFRLDLLANEGYL 442
Qy 121 NPQNDTVILRFQVRS 135
Db ||||||||||||||||
443 NPQNDTVILRFQVRS 457

Search completed: July 20, 2005, 20:47:42
Job time : 96.5357 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:00 ; Search time 19.2857 Seconds
(without alignments)
673.517 Million cell updates/sec

Title: US-09-706-325-25
Perfect score: 135
Sequence: 1 ELVPSYDSATFVLENFSTLR.....NEGYLNFQNDTVILRFQVRS 135

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

PIR_79:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	5.9	210	2	A69898
2	7	5.2	253	2	T36718
3	7	5.2	257	2	C72418
4	7	5.2	285	2	H75032
5	7	5.2	316	2	T27194
6	7	5.2	377	2	AC3426
7	7	5.2	444	2	T35794
8	7	5.2	507	2	T48645
9	7	5.2	507	2	AD1336
10	7	5.2	507	2	AB1707
11	7	5.2	512	2	G69670
12	7	5.2	548	2	E89910
13	7	5.2	727	2	C84534
14	7	5.2	818	2	F96586
15	7	5.2	904	2	T04377
16	7	5.2	1777	2	T00490
17	6	4.4	38	2	F36491
18	6	4.4	77	2	G90411
19	6	4.4	80	2	A60699
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21	6	4.4	89	2	D83372
22	6	4.4	98	2	T03585
23	6	4.4	101	2	T07828
24	6	4.4	102	2	F71354
25	6	4.4	112	2	C55993
26	6	4.4	115	2	T21833
27	6	4.4	120	2	PD0026
28	6	4.4	124	2	C70537
29	6	4.4	127	2	A64927

hypothetical prote
hypothetical prote
transcription regu
conserved hypothet
transcription regu
probable membrane
3-hydroxybutyryl-C
extensin - carrot
hypothetical prote
hypothetical prote
cysteine dioxygna
hypothetical prote
hypothetical prote
type 4 fimbrial bi
pilus assembly pro
senescence-associat
senescence-associat
hypothetical prote
hypothetical prote
hypothetical prote
tupR protein - Pee
resolvase - Escher
resolvase (EC 6.5.
fimbrial-like prot
probable fimbrial-
probable fimbrial-
hypothetical prote
hypothetical prote
probable signal se
protein-export pro
probable peptidyl-
maf protein (impor
probable peptidyl-
D83 protein (impor
hypothetical prote
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hypothetical prote
DNA-directed RNA p
unknown protein en
hypothetical prote
NADH dehydrogenase
probable transcrip
probable transmem
oxidoreductase, sh
hypothetical prote
probable adenosylh
5-methylthioadenos
FixK-like regulato
conserved hypothet
hypothetical prote
hypothetical prote
sulfate ABC transp
hypothetical prote
hypothetical prote
phosphonates trans
hypothetical prote
heat shock protein
type III export pr
transcription regu
hypothetical prote
probable amino aci
hypothetical prote
hypothetical prote
iron(iii) dicitrat
USF protein homolo
probable enoyl-CoA
hydroxyproline-ric
transcription facto
thua protein (impo
SAM-dependent meth
probable ARAC-type

103	6	4.4	274	2	B96024	probable ARAC-type	176	6	4.4	343	2	AF1783	polyol dehydrogena
104	6	4.4	274	2	S47736	probable transcrip	177	6	4.4	343	2	T19979	hypothetical prote
105	6	4.4	275	2	H86950	probable ABC-trans	178	6	4.4	344	2	H82656	twitching motility
106	6	4.4	277	2	AJ35955	probable transposo	179	6	4.4	344	2	JN0055	twitching motility
107	6	4.4	278	2	S20790	extensin - almond	180	6	4.4	345	2	S55969	H+-exporting ATPas
108	6	4.4	278	2	H96639	protein Tif9.4 [im	181	6	4.4	346	1	JH0387	alkanal monooxygen
109	6	4.4	279	2	E69595	transcription acti	182	6	4.4	346	2	D90244	hypothetical prote
110	6	4.4	283	2	C87346	hypothetical prote	183	6	4.4	346	2	G75486	probable type I to
111	6	4.4	285	2	H90488	arabinose ABC tran	184	6	4.4	350	2	T14191	extensin homolog 1
112	6	4.4	286	2	B70833	carbon-monoxide de	185	6	4.4	350	2	T25366	hypothetical prote
113	6	4.4	286	2	A84063	hypothetical prote	186	6	4.4	350	2	H86371	40.0K hypothetical
114	6	4.4	287	2	G86707	divalent cation tr	187	6	4.4	351	2	T101845	hypothetical prote
115	6	4.4	288	2	T22721	hypothetical prote	188	6	4.4	352	2	T10905	adenylate cyclase
116	6	4.4	289	2	A12179	hypothetical prote	189	6	4.4	359	2	JC5382	hereditary hemochr
117	6	4.4	291	1	NCBP75	phosphodiesterase	190	6	4.4	362	2	S68471	asparaginase (EC 3
118	6	4.4	291	2	D64377	ribosomal protein	191	6	4.4	362	2	C90674	hypothetical prote
119	6	4.4	292	2	H96784	hypothetical prote	192	6	4.4	363	2	T50582	FecCD-family membr
120	6	4.4	292	1	NMECMG	maltose transport	193	6	4.4	365	2	F85524	hypothetical prote
121	6	4.4	296	2	AB1014	maltose transport	194	6	4.4	368	2	G83015	3-dehydroquinatase
122	6	4.4	296	2	S05333	maltose transport	195	6	4.4	369	2	F83250	histidinol-phospha
123	6	4.4	296	2	C86096	part of maltose pe	196	6	4.4	370	2	S27344	hupK protein - Rhi
124	6	4.4	296	2	G91255	transport system p	197	6	4.4	370	2	A83621	probable ATP-bindi
125	6	4.4	296	2	A60175	maltose transport	198	6	4.4	372	2	B41874	heat shock protein
126	6	4.4	296	2	AD0452	maltose transport	199	6	4.4	372	2	AD2111	twitching motility
127	6	4.4	297	2	F87567	integral membrane	200	6	4.4	376	2	D72493	hypothetical prote
128	6	4.4	297	2	C83143	hypothetical prote	201	6	4.4	378	2	S25279	flagellar motor sw
129	6	4.4	299	2	S12022	extensin - rape	202	6	4.4	380	2	H81152	anticonodon nuclea
130	6	4.4	300	2	A70616	probable ephr prot	203	6	4.4	381	2	B84935	acetylornithine de
131	6	4.4	301	2	C69143	hypothetical prote	204	6	4.4	386	2	T12845	hypothetical prote
132	6	4.4	301	2	T52437	PRM1 homolog [impo	205	6	4.4	388	2	T32153	hypothetical prote
133	6	4.4	305	2	JC4920	2-oxoacid-faradox	206	6	4.4	390	2	T16782	hypothetical prote
134	6	4.4	305	2	B81426	methionyl-tRNA for	207	6	4.4	394	2	E83903	thiolase (acetyl-C
135	6	4.4	305	2	T34309	hypothetical prote	208	6	4.4	399	2	D86322	hypothetical prote
136	6	4.4	306	2	A24354	extensin precursor	209	6	4.4	400	2	T32705	hypothetical prote
137	6	4.4	307	2	S54080	carrier protein YM	210	6	4.4	405	2	C90194	hypothetical prote
138	6	4.4	308	2	H65035	hypothetical prote	211	6	4.4	411	2	D72588	hypothetical prote
139	6	4.4	308	2	C31059	probable transcrip	212	6	4.4	412	2	T30079	hypothetical prote
140	6	4.4	308	2	A85904	probable transcrip	213	6	4.4	412	2	JC1116	type III site-spec
141	6	4.4	310	2	T44857	probable hydroxyly	214	6	4.4	413	2	T26403	hypothetical prote
142	6	4.4	310	2	S12807	cnjC protein, conj	215	6	4.4	421	2	E96522	hypothetical prote
143	6	4.4	311	2	T32915	hypothetical prote	216	6	4.4	432	2	T35527	hypothetical prote
144	6	4.4	312	2	B69170	UDP-N-acetylmutam	217	6	4.4	433	2	D87636	amino acid permeas
145	6	4.4	312	2	AB1233	hypothetical prote	218	6	4.4	433	2	AH2169	sulfide-quinone re
146	6	4.4	313	2	D83961	malonyl CoA-acyl c	219	6	4.4	434	2	D86530	N utilization prot
147	6	4.4	313	2	G71886	hypothetical prote	220	6	4.4	434	2	E72093	N utilization subs
148	6	4.4	313	2	D64626	hypothetical prote	221	6	4.4	434	2	H81709	N utilization subs
149	6	4.4	313	2	AD1352	S. aureus Cbf1 pro	222	6	4.4	434	2	A71559	probable transcrip
150	6	4.4	315	2	B96533	hypothetical prote	223	6	4.4	438	1	S11225	transcription fact
151	6	4.4	316	2	F81330	hypothetical prote	224	6	4.4	438	2	S77655	hypothetical prote
152	6	4.4	316	2	T52464	hypothetical prote	225	6	4.4	439	2	E75118	probable threonine
153	6	4.4	316	2	B71082	hypothetical prote	226	6	4.4	440	1	A35875	transcription fact
154	6	4.4	318	2	H81255	hypothetical prote	227	6	4.4	440	2	I48291	transcription fact
155	6	4.4	318	2	G82350	lipid A biosynthes	228	6	4.4	440	2	AE1395	conserved hypoteth
156	6	4.4	320	2	F70034	conserved hypoteth	229	6	4.4	440	2	AH1770	conserved hypoteth
157	6	4.4	320	2	D97197	hypothetical prote	230	6	4.4	440	2	H71013	probable threonine
158	6	4.4	326	2	S36705	duRP diphosphatase	231	6	4.4	441	1	A53988	transcription fact
159	6	4.4	326	2	T42552	duRP diphosphatase	232	6	4.4	441	1	TVCHTE	transcription fact
160	6	4.4	326	2	S32585	structural prote-in	233	6	4.4	441	1	TVHUET	transcription fact
161	6	4.4	326	2	D95309	probable UDP-glucos	234	6	4.4	443	2	A99657	hypothetical prote
162	6	4.4	327	2	AH3216	UDP-glucose 4-epim	235	6	4.4	443	2	A85508	hypothetical prote
163	6	4.4	328	2	B59296	alpha-N-arabinofur	236	6	4.4	444	2	E83033	probable MFS trans
164	6	4.4	329	2	T24701	hypothetical prote	237	6	4.4	444	2	AH3613	hypothetical prote
165	6	4.4	329	2	C96033	probable regulator	238	6	4.4	446	2	G75304	conserved hypoteth
166	6	4.4	330	2	S22140	nodulin Enod2 - Se	239	6	4.4	448	1	H69032	polyferredoxin 2 -
167	6	4.4	331	2	A71338	conserved hypoteth	240	6	4.4	450	2	H81338	probable sugar tra
168	6	4.4	333	2	B86621	aspartate dehydrog	241	6	4.4	452	2	A82777	anthranilate synth
169	6	4.4	333	2	G72002	aspartate dehydrog	242	6	4.4	454	2	S75610	UDP-N-acetylmuram
170	6	4.4	333	2	T01846	hypothetical prote	243	6	4.4	458	2	A83391	probable glutamine
171	6	4.4	335	2	B75091	pyruvate formate-l	244	6	4.4	458	2	B83609	probable glutamine
172	6	4.4	337	1	B71052	hypothetical prote	245	6	4.4	458	2	C86860	hypothetical prote
173	6	4.4	341	2	G86315	hypothetical prote	246	6	4.4	458	2	C97151	hypothetical prote
174	6	4.4	342	2	AC3274	hydroxymethylbilan	247	6	4.4	461	2	G75598	acetyl-CoA acetyl
175	6	4.4	343	2	AF1407	polyol dehydrogena	248	6	4.4	462	1	JC4686	juvenile-hormone e

249	6	4.4	463	2	D88104	protein W10G11.19	322	6	4.4	564	2	S06896	nucleocapsid prote
250	6	4.4	466	2	Af2274	hypothetical prote	323	6	4.4	568	2	S28089	hypothetical prote
251	6	4.4	468	2	B87158	PPF-family protein	324	6	4.4	570	2	C97408	long-chain-fatty-a
252	6	4.4	470	1	S56565	hypothetical 53K p	325	6	4.4	570	2	AD2626	long-chain-fatty-a
253	6	4.4	470	2	F31291	probable regulator	326	6	4.4	572	2	S64387	protein kinase DBF
254	6	4.4	470	2	H86132	probable regulator	327	6	4.4	573	2	B70726	probable secd - My
255	6	4.4	472	1	A53236	transcription fact	328	6	4.4	573	2	B70942	hypothetical prote
256	6	4.4	473	2	JH0754	sucrose-6-phosphat	329	6	4.4	576	2	T48573	hypothetical prote
257	6	4.4	473	2	D88976	protein P54E2.4 [i	330	6	4.4	581	2	A97119	probable membrane
258	6	4.4	475	2	T24900	hypothetical prote	331	6	4.4	583	2	C84749	hypothetical prote
259	6	4.4	477	2	AG0905	RNA polymerase sig	332	6	4.4	586	1	S34731	amylase [EC 3.2.1.
260	6	4.4	477	2	A35695	transcription init	333	6	4.4	587	2	AG3019	conserved hypothet
261	6	4.4	477	2	D85984	RNA polymerase sig	334	6	4.4	592	2	T21536	hypothetical prote
262	6	4.4	477	2	A98139	RNA polymerase sig	335	6	4.4	602	2	D75618	hypothetical prote
263	6	4.4	477	2	A24115	transcription init	336	6	4.4	602	2	E90568	DNA primase [impor
264	6	4.4	477	2	A1026	regulatory protein	337	6	4.4	603	2	S06059	gene ND1 intron 4
265	6	4.4	477	2	S62824	preprotein translo	338	6	4.4	605	2	T39837	dnak-type molecula
266	6	4.4	480	2	G70678	hypothetical prote	339	6	4.4	607	2	T20796	hypothetical prote
267	6	4.4	481	2	S11979	threonine synthase	340	6	4.4	614	2	T20795	hypothetical prote
268	6	4.4	481	2	A89102	protein P25E5.4 [i	341	6	4.4	615	2	F64572	arginine decarboxy
269	6	4.4	481	2	B70908	hypothetical prote	342	6	4.4	615	2	C71867	arginine decarboxy
270	6	4.4	485	1	TVCHET	transcription fact	343	6	4.4	618	2	B64564	transketolase B -
271	6	4.4	486	2	Af1575	acetaldehyde dehyd	344	6	4.4	618	2	H71946	1-deoxyxylulose-5-
272	6	4.4	486	2	AC1222	acetaldehyde dehyd	345	6	4.4	620	2	S06733	hydroxyproline-ric
273	6	4.4	487	2	T21645	hypothetical prote	346	6	4.4	628	2	AB0548	PrpE protein [impo
274	6	4.4	488	1	TVFVES	transcription fact	347	6	4.4	634	2	B98265	hypothetical prote
275	6	4.4	491	1	JN0491	X-Pro aminopeptida	348	6	4.4	638	2	A82260	penicillin-binding
276	6	4.4	491	1	CEECAM	UDP-N-acetylmuram	349	6	4.4	638	2	AH0340	putative autotransp
277	6	4.4	491	2	AF0518	UDP-N-acetyl-muram	350	6	4.4	645	2	H70173	probable long-chai
278	6	4.4	491	2	G85491	UDP-N-acetyl-muram	351	6	4.4	646	2	T47154	hypothetical prote
279	6	4.4	491	2	G90640	UDP-N-acetyl-muram	352	6	4.4	646	2	G84854	hypothetical prote
280	6	4.4	491	2	A10068	UDP-N-acetyl-muram	353	6	4.4	647	2	B34457	204 protein - mous
281	6	4.4	491	2	B96633	hypothetical prote	354	6	4.4	654	2	B84017	hypothetical prote
282	6	4.4	492	2	T43346	nuclear receptor N	355	6	4.4	657	2	B84869	probable Sfl6 prot
283	6	4.4	494	2	H75587	conserved hypothet	356	6	4.4	672	2	G87386	protein-glutamine
284	6	4.4	496	2	C87194	probable transmemb	357	6	4.4	680	2	JC5133	hypothetical prote
285	6	4.4	497	1	S31337	glucose-6-phosphat	358	6	4.4	684	2	T48357	hypothetical prote
286	6	4.4	498	1	D71179	probable sugar ABC	359	6	4.4	687	2	D84126	penicillin-binding
287	6	4.4	498	2	E72493	probable ribose AB	360	6	4.4	692	2	AD1857	hypothetical prote
288	6	4.4	498	2	H75161	ribose abc transpo	361	6	4.4	694	2	T01005	hypothetical prote
289	6	4.4	499	2	H70453	virulence factor M	362	6	4.4	695	2	T52429	PRM1 homolog [impo
290	6	4.4	500	2	S16788	probable reverse t	363	6	4.4	696	2	G71829	probable outer mem
291	6	4.4	508	2	A72201	UDP-sugar diphosph	364	6	4.4	699	1	XEBYUG	UDPglucose 4-epime
292	6	4.4	514	1	B31997	IMP dehydrogenase	365	6	4.4	699	2	T05225	extensin homolog F
293	6	4.4	514	1	A31997	IMP dehydrogenase	366	6	4.4	706	2	G82943	hypothetical UU029
294	6	4.4	514	1	J70565	IMP dehydrogenase	367	6	4.4	713	2	T40051	hypothetical prote
295	6	4.4	518	2	A12426	hypothetical prote	368	6	4.4	721	2	T40317	actin-like protein
296	6	4.4	519	2	B87233	probable secreted	369	6	4.4	722	2	E71403	hypothetical prote
297	6	4.4	520	2	T14752	microphthalmia-ass	370	6	4.4	726	2	S62180	nuclear pore prote
298	6	4.4	523	1	S30805	probable RNA helic	371	6	4.4	732	1	S23864	translation elonga
299	6	4.4	523	2	D93631	probable sulfate t	372	6	4.4	735	2	S57486	ferrihyrogobactin
300	6	4.4	525	2	A96183	D-ribulokinase [EC	373	6	4.4	735	2	T50068	probable ATP-depen
301	6	4.4	525	2	A31303	ribitol kinase [im	374	6	4.4	743	2	E71432	hypothetical prote
302	6	4.4	528	2	G90569	hypothetical prote	375	6	4.4	752	2	G85941	hypothetical prote
303	6	4.4	529	1	M2EC8	58K mobilization p	376	6	4.4	752	2	C91096	hypothetical prote
304	6	4.4	529	2	S51477	extracellular glyc	377	6	4.4	752	2	B65070	probable oxidoredu
305	6	4.4	530	2	A18335	methionyl-tRNA syn	378	6	4.4	753	2	A96747	probable RNA-bindi
306	6	4.4	535	2	C83395	probable acyl-CoA	379	6	4.4	756	2	S74742	exopolysaccharide
307	6	4.4	536	2	T04234	calmodulin-binding	380	6	4.4	760	2	T06291	extensin homolog T
308	6	4.4	540	2	JC4916	signal transducing	381	6	4.4	773	2	T44989	transducer protein
309	6	4.4	541	2	T33583	hypothetical prote	382	6	4.4	775	2	S45495	isp4 protein - fis
310	6	4.4	543	1	ERADDC	fiber protein - ca	383	6	4.4	789	2	S46631	aconitate hydratase
311	6	4.4	544	2	T13877	NAHD2 dehydrogenas	384	6	4.4	807	2	F85647	probable outer mem
312	6	4.4	544	2	S54531	hypothetical prote	385	6	4.4	807	2	F64844	ydcS protein precu
313	6	4.4	550	2	S25202	spiramycin-resista	386	6	4.4	807	2	F90787	probable outer mem
314	6	4.4	551	2	B64005	hypothetical prote	387	6	4.4	811	2	E97040	phage related prot
315	6	4.4	551	2	D83277	electron transfer	388	6	4.4	822	2	T41941	glycoprotein B - h
316	6	4.4	552	2	T28752	phenylalanine-tRNA	389	6	4.4	830	2	T36683	probable integral
317	6	4.4	552	2	S48328	hypothetical prote	390	6	4.4	832	2	S19418	probable membrane
318	6	4.4	560	2	T08750	hypothetical prote	391	6	4.4	837	2	H84239	dimethylsulfoxide
319	6	4.4	564	1	VHXPUV	major structural n	392	6	4.4	842	2	S18462	glycoprotein H pre
320	6	4.4	564	1	VHXPMV	major structural n	393	6	4.4	847	2	F96531	hypothetical prote
321	6	4.4	564	2	S12480	nucleocapsid prote	394	6	4.4	876	2	G90592	hypothetical prote

395	6	4.4	886	2	S48371	hypothetical prote	468	6	4.4	2475	2	T00047	gellan lyase (EC 4
396	6	4.4	887	2	S57430	probable format d	469	6	4.4	2489	2	S59782	probable membrane
397	6	4.4	892	2	T27005	hypothetical prote	470	6	4.4	2809	2	T30213	g-cadherin - sea u
398	6	4.4	895	2	T32374	hypothetical prote	471	6	4.4	3083	2	AH2493	hypothetical prote
399	6	4.4	899	2	H96617	probable disease r	472	6	4.4	3535	2	E83641	probable hemagglut
400	6	4.4	899	2	B48586	suppressor of hair	473	6	4.4	3746	1	YGPLV3	alpha-aminoadipyl-
401	6	4.4	900	2	G96617	probable disease r	474	6	4.4	3791	1	YGPLV8	alpha-aminoadipyl-
402	6	4.4	900	2	S66264	55.11 protein homo	475	6	4.4	5627	2	C83339	hypothetical prote
403	6	4.4	906	2	S62667	protein translocas	476	6	4.4	6658	2	T13931	projectin - fruit
404	6	4.4	913	2	E75554	valyl-tRNA synthet	477	5	3.7	14	1	LFEBWC	trp operon leader
405	6	4.4	946	2	S28061	SCP1 protein - rat	478	5	3.7	17	2	A27486	folitropin inhibi
406	6	4.4	947	2	I49635	mouse Dhml protein	479	5	3.7	21	2	FC1310	small granule S3 c
407	6	4.4	956	2	G70327	isoleucine-tRNA li	480	5	3.7	33	2	H82078	hypothetical prote
408	6	4.4	958	2	C86308	F20D23.9 protein -	481	5	3.7	34	2	C44336	neurotoxin Tx3-3 -
409	6	4.4	967	2	S68852	hypothetical prote	482	5	3.7	35	2	JQ2193	hypothetical 3.9K
410	6	4.4	1012	2	B97326	endoglucanase fami	483	5	3.7	36	2	A37172	collagen alpha 1(X
411	6	4.4	1020	2	B82427	sensor protein Tor	484	5	3.7	37	2	A82057	ribosomal protein
412	6	4.4	1024	2	S71804	receptor-like serp	485	5	3.7	38	2	AG0028	50S ribosomal prot
413	6	4.4	1024	2	A83557	acriflavin resista	486	5	3.7	43	2	T33020	hypothetical prote
414	6	4.4	1035	1	A43090	enteropeptidase (E	487	5	3.7	44	2	T18729	hypothetical prote
415	6	4.4	1036	2	D70117	acriflavine resist	488	5	3.7	44	2	B46078	hypothetical prote
416	6	4.4	1046	2	F71432	hypothetical prote	489	5	3.7	45	2	B83689	hypothetical prote
417	6	4.4	1048	2	S64758	SCD25 protein (ver	490	5	3.7	46	2	C82345	hypothetical prote
418	6	4.4	1048	2	T31653	hypothetical prote	491	5	3.7	46	2	A71571	hypothetical prote
419	6	4.4	1087	2	C84263	transmembrane olig	492	5	3.7	49	2	S11814	opacity protein (c
420	6	4.4	1095	2	I49270	Na+/K+/Cl-cotransp	493	5	3.7	51	2	F90802	hypothetical prote
421	6	4.4	1095	2	A54145	sodium-potassium-c	494	5	3.7	51	2	E85662	hypothetical prote
422	6	4.4	1099	2	I46498	bumetanide-sensiti	495	5	3.7	52	2	I40664	hook protein - Cau
423	6	4.4	1108	2	AF1047	probable membrane	496	5	3.7	53	2	S77936	exoskeletal protei
424	6	4.4	1112	2	H95964	probable outer mem	497	5	3.7	53	2	AF1734	hypothetical prote
425	6	4.4	1117	2	T19727	hypothetical prote	498	5	3.7	54	2	H82450	hypothetical prote
426	6	4.4	1127	2	S97580	hypothetical prote	499	5	3.7	56	1	ERBF1B	gene 1B protein -
427	6	4.4	1131	2	T15787	hypothetical prote	500	5	3.7	56	2	AB1818	hypothetical prote
428	6	4.4	1170	2	S52525	probable membrane	501	5	3.7	57	2	JC5008	hypothetical prote
429	6	4.4	1189	2	T30319	Lian-Aal retrotran	502	5	3.7	57	2	D84196	protein translocas
430	6	4.4	1191	2	S76414	beta transducin-li	503	5	3.7	57	2	G97910	hypothetical prote
431	6	4.4	1202	2	T37867	hypothetical prote	504	5	3.7	57	2	AH0423	probable membrane
432	6	4.4	1204	2	C75015	probable pyrolysein	505	5	3.7	59	2	T07299	NADH dehydrogenase
433	6	4.4	1213	2	T41378	probable helicase	506	5	3.7	59	2	A69520	hypothetical prote
434	6	4.4	1225	2	A56514	chromokinesin - ch	507	5	3.7	60	2	E35156	thioredoxin-disulf
435	6	4.4	1236	2	T70977	hypothetical prote	508	5	3.7	60	2	D84173	hypothetical prote
436	6	4.4	1236	2	T19492	hypothetical prote	509	5	3.7	62	2	C90761	probable division
437	6	4.4	1250	2	S14177	SCD25 protein (ver	510	5	3.7	62	2	H85624	hypothetical prote
438	6	4.4	1286	1	S38058	hypothetical prote	511	5	3.7	62	2	S73032	hypothetical prote
439	6	4.4	1297	2	T39287	hypothetical prote	512	5	3.7	62	2	T14430	chromomethylase CM
440	6	4.4	1322	2	T24140	hypothetical prote	513	5	3.7	64	2	G97027	hypothetical prote
441	6	4.4	1328	2	T23007	hypothetical prote	514	5	3.7	65	2	C86210	protein P22G5.4 [i
442	6	4.4	1353	2	T00249	ich1 protein - ink	515	5	3.7	65	2	F83727	hypothetical prote
443	6	4.4	1378	2	T47605	RING finger-like p	516	5	3.7	66	2	S47027	DNA-directed RNA p
444	6	4.4	1382	2	T01789	protoporphyrin IX	517	5	3.7	67	2	G81110	hypothetical prote
445	6	4.4	1383	2	T07126	magnesium chelatas	518	5	3.7	68	1	JN0537	head protein gp3 -
446	6	4.4	1408	2	T43261	multidrug resistan	519	5	3.7	68	2	F90970	probable head comp
447	6	4.4	1431	2	A45866	dextranucrase (EC	520	5	3.7	68	2	JC4271	hypothetical 7.5k
448	6	4.4	1541	2	T30227	pipecolate-incorpo	521	5	3.7	69	2	E69169	hypothetical prote
449	6	4.4	1582	2	A56248	sulfonylurea recep	522	5	3.7	70	2	T14901	chlorismate mutase
450	6	4.4	1616	2	E90704	Rns core protein w	523	5	3.7	70	2	F72280	conserved hypotnet
451	6	4.4	1645	2	H85554	hypothetical prote	524	5	3.7	70	2	S76907	hypothetical prote
452	6	4.4	1651	2	F88750	protein vit-6 [imp	525	5	3.7	72	2	AE1038	hypothetical prote
453	6	4.4	1651	2	B43081	vitellogenin vit-6	526	5	3.7	72	2	T17937	hypothetical prote
454	6	4.4	1660	2	T18561	vitellogenin vit-6	527	5	3.7	72	2	B81034	hypothetical prote
455	6	4.4	1694	2	A83512	hypothetical prote	528	5	3.7	72	2	C75519	hypothetical prote
456	6	4.4	1742	2	S24600	projectin - fruit	529	5	3.7	72	2	T11975	hypothetical prote
457	6	4.4	1747	2	T43162	vitellogenin - gyp	530	5	3.7	72	2	T25597	hypothetical prote
458	6	4.4	1767	2	H97912	conserved hypotnet	531	5	3.7	73	2	G87164	hypothetical prote
459	6	4.4	1784	2	C96615	hypothetical prote	532	5	3.7	74	2	S13515	retinoic acid rece
460	6	4.4	1807	2	JC6319	integrin beta-4 ch	533	5	3.7	75	2	F75031	hydrogenase expres
461	6	4.4	1871	2	D86698	probable DNA polym	534	5	3.7	75	2	F75345	hypothetical prote
462	6	4.4	1894	2	T02155	DNA-directed DNA p	535	5	3.7	75	2	F97837	proline/betaine tr
463	6	4.4	2078	2	T25400	hypothetical prote	536	5	3.7	75	2	AE1588	hypothetical prote
464	6	4.4	2163	2	T15276	hypothetical prote	537	5	3.7	75	2	AF1651	hypothetical prote
465	6	4.4	2201	2	A54774	ATP binding casset	538	5	3.7	76	2	H81214	hypothetical prote
466	6	4.4	2271	2	F90073	hypothetical prote	539	5	3.7	76	2	S72752	B1496 Cl 130 prote
467	6	4.4	2298	2	T49648	hypothetical prote	540	5	3.7	76	2	T24627	hypothetical prote

541	5	3.7	76	2	G82544	hypothetical prote	614	5	3.7	105	2	T31300	hypothetical prote
542	5	3.7	77	2	S36032	hemadin precursor	615	5	3.7	105	2	T14666	hypothetical prote
543	5	3.7	77	2	A05190	hypothetical prote	616	5	3.7	105	2	AD2633	hypothetical prote
544	5	3.7	77	2	G36769	17R protein - huma	617	5	3.7	106	2	S69868	hypothetical prote
545	5	3.7	80	2	A01906	hypothetical prote	618	5	3.7	106	2	D72476	hypothetical prote
546	5	3.7	80	2	C82761	hypothetical prote	619	5	3.7	106	2	E97727	hypothetical prote
547	5	3.7	82	2	D4562	hypothetical prote	620	5	3.7	106	2	C81988	hypothetical prote
548	5	3.7	82	2	T18159	hypothetical prote	621	5	3.7	106	2	J00234	hypothetical 12.5K
549	5	3.7	82	2	T10869	y4KO protein - Rhi	622	5	3.7	107	1	SSUL	stellacyanin - Jap
550	5	3.7	83	2	A82906	hypothetical prote	623	5	3.7	107	2	AB1051	hypothetical prote
551	5	3.7	83	2	T07252	hypothetical prote	624	5	3.7	107	2	S53575	probable membrane
552	5	3.7	83	2	D84697	hypothetical prote	625	5	3.7	107	2	A44355	Cu44 glycoprotein
553	5	3.7	83	2	T18171	hypothetical prote	626	5	3.7	107	2	B31915	hypothetical prote
554	5	3.7	85	2	G69207	thioredoxin - Meth	627	5	3.7	108	2	AD2458	hypothetical prote
555	5	3.7	85	2	H84728	hypothetical prote	628	5	3.7	108	1	D71209	ribosomal protein
556	5	3.7	85	2	T18143	hypothetical prote	629	5	3.7	109	2	JC2440	biphenyl dioxygena
557	5	3.7	85	2	F96949	hypothetical prote	630	5	3.7	109	2	C31183	photosystem II pro
558	5	3.7	86	2	D33989	Ig heavy chain V-4	631	5	3.7	109	2	S69581	hypothetical prote
559	5	3.7	86	2	T31846	hypothetical prote	632	5	3.7	109	2	A72546	hypothetical prote
560	5	3.7	86	2	A10179	hypothetical prote	633	5	3.7	109	2	G81244	pHnA protein NMB00
561	5	3.7	87	2	S41306	hypothetical prote	634	5	3.7	109	2	F82023	pHnA protein homol
562	5	3.7	87	2	S44877	ZC21.5 protein - C	635	5	3.7	109	2	B70037	hypothetical prote
563	5	3.7	89	2	T43992	hypothetical prote	636	5	3.7	109	2	T29794	hypothetical prote
564	5	3.7	89	2	A64651	conserved hypotHet	637	5	3.7	109	2	C84386	hypothetical prote
565	5	3.7	89	2	D71940	hypothetical prote	638	5	3.7	110	2	AE2282	mutator MutT prote
566	5	3.7	89	2	AG3394	hypothetical membr	639	5	3.7	110	2	C64598	hypothetical prote
567	5	3.7	90	2	JR0210	proteinase (BC 3.4	640	5	3.7	111	1	JC7085	ferredoxin [2Fe-2S
568	5	3.7	91	2	S25462	Ig kappa chain V r	641	5	3.7	111	2	B75084	hypothetical prote
569	5	3.7	92	1	RSHER	ribosomal protein	642	5	3.7	111	2	T36555	probable membrane
570	5	3.7	92	1	A05074	macrophage inflam	643	5	3.7	111	2	B84046	hypothetical prote
571	5	3.7	92	2	I54781	fibroblast growth	644	5	3.7	111	2	AF0139	probable starvatio
572	5	3.7	92	2	A86197	protein F9P14.1 [i	645	5	3.7	112	2	S48974	hypothetical prote
573	5	3.7	92	2	G69454	hypothetical prote	646	5	3.7	112	2	JC2020	peptide transporte
574	5	3.7	93	2	C35673	LD78-beta protein	647	5	3.7	112	2	B24773	protein-tyrosine k
575	5	3.7	94	1	F75022	ribosomal protein	648	5	3.7	112	2	AE0451	hypothetical prote
576	5	3.7	94	2	S10732	hypothetical prote	649	5	3.7	113	1	Q0ECXQ	hypothetical prote
577	5	3.7	94	2	G86658	hypothetical prote	650	5	3.7	113	2	C24773	protein-tyrosine k
578	5	3.7	94	2	H75341	hypothetical prote	651	5	3.7	113	2	S16254	hypothetical prote
579	5	3.7	94	2	C97048	hypothetical prote	652	5	3.7	113	2	AD1039	hypothetical prote
580	5	3.7	95	1	WSL15B	E5B protein - bovi	653	5	3.7	113	2	AB1646	hypothetical prote
581	5	3.7	95	2	A56644	inverted repeat co	654	5	3.7	113	2	T35806	hypothetical prote
582	5	3.7	95	2	F83887	hypothetical prote	655	5	3.7	114	2	F83959	ribosomal protein
583	5	3.7	95	2	S84537	probable membrane	656	5	3.7	114	2	JC5482	hypothetical 13.2K
584	5	3.7	95	2	E81360	probable periplasm	657	5	3.7	114	2	F90557	hypothetical prote
585	5	3.7	96	2	S49377	translation releas	658	5	3.7	114	2	B84710	hypothetical prote
586	5	3.7	96	2	A64606	hypothetical prote	659	5	3.7	114	2	S77051	transposase sil066
587	5	3.7	96	2	S69798	holin protein, 10.	660	5	3.7	115	2	B83407	hypothetical prote
588	5	3.7	97	1	A47365	defensin alpha-4 p	661	5	3.7	115	2	AH1891	hypothetical prote
589	5	3.7	98	2	S68136	NADH2 dehydrogenas	662	5	3.7	116	1	THUAP	glycoprotein hormo
590	5	3.7	98	2	B64360	hypothetical prote	663	5	3.7	116	2	S76118	hypothetical prote
591	5	3.7	99	1	QQYBW	hypothetical prote	664	5	3.7	116	2	A12039	hypothetical prote
592	5	3.7	99	2	D30484	hypothetical prote	665	5	3.7	116	2	B64451	hypothetical prote
593	5	3.7	99	2	T39208	very hypothetical	666	5	3.7	117	2	T47990	hypothetical prote
594	5	3.7	99	2	T01678	hypothetical prote	667	5	3.7	117	2	AB2757	hypothetical prote
595	5	3.7	100	2	E96121	cytochrome b (562)	668	5	3.7	118	2	CH2967	6-pyruvoyltetrahyd
596	5	3.7	100	2	S86121	hypothetical prote	669	5	3.7	118	2	C98315	exsC protein (AJ22
597	5	3.7	100	2	S37793	hypothetical prote	670	5	3.7	118	2	S49946	probable membrane
598	5	3.7	100	2	S89744	hypothetical prote	671	5	3.7	118	2	T35739	probable integral
599	5	3.7	100	2	A82479	hypothetical prote	672	5	3.7	118	2	T17380	vIAA protein - Dic
600	5	3.7	101	2	S69300	hypothetical prote	673	5	3.7	118	2	AF2022	hypothetical prote
601	5	3.7	101	2	A88500	protein K04G7.12 [674	5	3.7	118	2	AG1004	conserved hypotHet
602	5	3.7	101	2	D83375	hypothetical prote	675	5	3.7	118	2	B64630	hypothetical prote
603	5	3.7	101	2	H81352	small hydrophobic	676	5	3.7	118	2	T27456	hypothetical prote
604	5	3.7	102	2	A11153	PTS system, fructo	677	5	3.7	119	2	H83744	hypothetical prote
605	5	3.7	102	2	A75417	hypothetical prote	678	5	3.7	119	2	AC1161	Chemotaxis respons
606	5	3.7	102	2	H70973	hypothetical prote	679	5	3.7	119	2	AC1520	Chemotaxis respons
607	5	3.7	103	2	D82165	hypothetical prote	680	5	3.7	119	2	F81735	conserved hypotHet
608	5	3.7	104	1	BVECAA	artA protein - Bsc	681	5	3.7	119	2	D71473	probable ioJap - C
609	5	3.7	104	2	S04719	ribosomal protein	682	5	3.7	119	2	G85998	hypothetical prote
610	5	3.7	104	2	T13549	hypothetical prote	683	5	3.7	119	2	C65128	hypothetical prote
611	5	3.7	104	2	B69058	hypothetical prote	684	5	3.7	119	2	C91153	hypothetical prote
612	5	3.7	104	2	H69261	hypothetical prote	685	5	3.7	119	2	AF3411	phosphohydrolase (
613	5	3.7	105	2	H87543	conserved hypotHet	686	5	3.7	120	1	UTPGA	glycoprotein hormo

687	5	3.7	120	2	C91027	D-erythro-7,8-dihy	760	5	3.7	130	2	AH2381	glycine cleavage s
688	5	3.7	120	2	B65002	D-erythro-7,8-dihy	761	5	3.7	130	2	AH1125	hypothetical prote
689	5	3.7	120	2	D85871	D-erythro-7,8-dihy	762	5	3.7	130	2	AG1486	hypothetical prote
690	5	3.7	120	2	I51241	pituitary glycopro	763	5	3.7	131	1	SIPSDP	steroid Delta-iso
691	5	3.7	120	2	A45585	glycoprotein hormo	764	5	3.7	131	2	H82337	preprotein translo
692	5	3.7	120	2	G00021	chlorionic gonadotr	765	5	3.7	131	2	S65197	probable membrane
693	5	3.7	120	2	A39555	glycoprotein hormo	766	5	3.7	131	2	T01487	hypothetical prote
694	5	3.7	120	2	S53062	glycoprotein hormo	767	5	3.7	132	1	JVB9PL	DNA-packaging prot
695	5	3.7	120	2	C29585	homeotic protein H	768	5	3.7	132	2	E90900	probable DNA-packa
696	5	3.7	120	2	T17514	hypothetical prote	769	5	3.7	132	2	D90833	DNA packaging prot
697	5	3.7	120	2	A87594	bleomycin resistan	770	5	3.7	132	2	AE0224	flagellar protein
698	5	3.7	120	2	AF0299	probable membrane	771	5	3.7	132	2	S04830	regulatory protein
699	5	3.7	120	2	A13137	hypothetical prote	772	5	3.7	132	2	G72774	hypothetical prote
700	5	3.7	120	2	D90546	proline dipeptidas	773	5	3.7	132	2	D87574	unknown protein, 4
701	5	3.7	120	2	B70187	ribosomal protein	774	5	3.7	132	2	H86416	probable auxin-ind
702	5	3.7	121	2	S06615	chorion protein s1	775	5	3.7	132	2	C86417	hypothetical prote
703	5	3.7	121	2	D97840	hypothetical prote	776	5	3.7	132	2	I40566	hypothetical prote
704	5	3.7	122	2	YLHUA	serum amyloid A2 p	777	5	3.7	133	2	T04081	probable ribosomal
705	5	3.7	122	1	YLHUS	serum amyloid A1 p	778	5	3.7	133	2	A44870	fatty acid-binding
706	5	3.7	122	2	D41287	Ig heavy chain V-I	779	5	3.7	133	2	C85583	probable tail comp
707	5	3.7	122	2	I39456	serum amyloid A2-b	780	5	3.7	133	2	A90733	probable minor tai
708	5	3.7	122	2	B72637	hypothetical prote	781	5	3.7	133	2	B84101	flagellar protein
709	5	3.7	122	2	E72584	hypothetical prote	782	5	3.7	133	2	T23921	hypothetical prote
710	5	3.7	122	2	T17850	hypothetical prote	783	5	3.7	133	2	JC2007	differentiation in
711	5	3.7	122	2	T40756	hypothetical prote	784	5	3.7	133	2	B86754	prophage pi2 prote
712	5	3.7	122	2	B90760	hypothetical prote	785	5	3.7	133	2	A86418	probable auxin-ind
713	5	3.7	122	2	E84837	hypothetical prote	786	5	3.7	133	2	A29174	clostripain (EC 3.
714	5	3.7	122	2	H85623	ycv protein - Esc	787	5	3.7	133	2	A82656	hypothetical prote
715	5	3.7	122	2	A05175	hypothetical prote	788	5	3.7	133	2	B97270	CBS domain contain
716	5	3.7	122	4	UN0029	serum amyloid A3 p	789	5	3.7	133	2	AH2580	PTS system, IIA co
717	5	3.7	123	2	T14949	hypothetical prote	790	5	3.7	133	2	F97362	PTS enzyme IIAB, m
718	5	3.7	123	2	H72479	probable translati	791	5	3.7	133	2	AE1971	hypothetical prote
719	5	3.7	124	2	T09855	acetyl-CoA carboxy	792	5	3.7	134	2	SI4076	Ig kappa chain - A
720	5	3.7	124	2	H72766	hypothetical prote	793	5	3.7	134	2	S43470	fatty-acid-binding
721	5	3.7	124	2	H72496	hypothetical prote	794	5	3.7	134	2	AD0323	NrdI protein homol
722	5	3.7	124	2	A83505	hypothetical prote	795	5	3.7	134	2	F84174	hypothetical prote
723	5	3.7	124	2	H86143	hypothetical prote	796	5	3.7	134	2	A40227	transcription repr
724	5	3.7	124	2	A72587	hypothetical prote	797	5	3.7	134	2	JC2112	helix-loop-helix p
725	5	3.7	125	2	F96973	transcription regu	798	5	3.7	135	2	H71499	hypothetical prote
726	5	3.7	125	2	B72517	hypothetical prote	799	5	3.7	135	2	C95375	hypothetical prote
727	5	3.7	125	2	D75313	hypothetical prote	800	5	3.7	135	2	H84968	flagella synthesis
728	5	3.7	125	2	C75507	hypothetical prote	801	5	3.7	135	2	H86417	probable auxin-ind
729	5	3.7	126	2	T00310	transposase - Esch	802	5	3.7	136	2	B65210	YjBA protein - Esc
730	5	3.7	126	2	A82575	hypothetical prote	803	5	3.7	136	2	T23859	hypothetical prote
731	5	3.7	127	2	B82817	translation initia	804	5	3.7	136	2	B96504	protein F9C16.21 l
732	5	3.7	127	2	T03866	hypothetical prote	805	5	3.7	136	2	F84890	hypothetical prote
733	5	3.7	127	2	A10894	probable exported	806	5	3.7	136	2	T32161	hypothetical prote
734	5	3.7	127	2	T07301	cell division topo	807	5	3.7	136	2	B97386	hypothetical prote
735	5	3.7	127	2	G72604	hypothetical prote	808	5	3.7	137	1	S25968	succinate dehydrog
736	5	3.7	127	2	D97449	hypothetical prote	809	5	3.7	137	2	D24773	protein-tyrosine k
737	5	3.7	127	2	AG2667	conserved hypothet	810	5	3.7	137	2	S43885	3-isopropylmalate
738	5	3.7	127	2	A83162	hypothetical prote	811	5	3.7	137	2	JQ2325	virion protein - A
739	5	3.7	127	2	A11362	hypothetical prote	812	5	3.7	137	2	A45355	ORF7 protein - Aut
740	5	3.7	127	2	PN0464	hypothetical prote	813	5	3.7	137	2	G81659	hypothetical prote
741	5	3.7	127	2	A48420	pheromone 4 praeur	814	5	3.7	137	2	H90342	hypothetical prote
742	5	3.7	128	1	C8EC62	cytochrome b562 pr	815	5	3.7	138	2	S36567	E6 protein - human
743	5	3.7	128	2	AF1056	soluble cytochrome	816	5	3.7	138	2	D85665	hypothetical prote
744	5	3.7	128	2	D64607	diacylglycerol kin	817	5	3.7	138	2	G70784	curli assembly/tra
745	5	3.7	128	2	G72763	hypothetical prote	818	5	3.7	138	2	G90805	curli assembly/tra
746	5	3.7	128	2	A70112	hypothetical prote	819	5	3.7	138	2	F98236	ornithine cyclodea
747	5	3.7	128	2	H65171	hypothetical trans	820	5	3.7	139	2	B97709	hypothetical prote
748	5	3.7	128	2	G31250	hypothetical prote	821	5	3.7	139	2	D86417	probable auxin-ind
749	5	3.7	128	2	B72600	hypothetical prote	822	5	3.7	139	2	E96030	conserved hypothet
750	5	3.7	128	2	A83492	hypothetical prote	823	5	3.7	140	2	S54215	flhE protein - Yer
751	5	3.7	129	2	S78153	ribosomal protein	824	5	3.7	140	2	AF0218	flagellar protein
752	5	3.7	129	2	A81980	hypothetical prote	825	5	3.7	140	2	S43789	probable cell wall
753	5	3.7	129	2	S73744	Mg296 homolog A05	826	5	3.7	140	2	D84594	hypothetical prote
754	5	3.7	129	2	AH2003	hypothetical prote	827	5	3.7	140	2	F86686	conserved hypothet
755	5	3.7	129	2	A82728	hypothetical prote	828	5	3.7	140	2	T35301	hypothetical prote
756	5	3.7	129	2	E84564	hypothetical prote	829	5	3.7	141	2	S31685	Ig heavy chain V r
757	5	3.7	129	2	T35391	probable transcrip	830	5	3.7	141	2	A91249	probable transcrip
758	5	3.7	129	2	T28983	hypothetical prote	831	5	3.7	141	2	T35223	probable ATP/Grp b
759	5	3.7	129	2	F72425	2-amino-4-hydroxy-	832	5	3.7	141	2	T13642	probable holin - S

833	5	3.7	141	2	AB0042	probable exported	906	5	3.7	151	2	C75157	protein tyrosine p
834	5	3.7	141	2	A70650	hypothetical prote	907	5	3.7	152	2	D82911	probable H1T prote
835	5	3.7	142	2	S73213	ribosomal protein	908	5	3.7	152	2	A95883	probable aldehyde
836	5	3.7	142	2	S73171	lsu ribosomal prot	909	5	3.7	152	2	T11658	mitochondrial impo
837	5	3.7	142	2	B71043	probable ribosomal	910	5	3.7	153	2	T04614	hypothetical prote
838	5	3.7	142	2	B75463	conserved hypothet	911	5	3.7	153	2	G82778	hypothetical prote
839	5	3.7	142	2	C75344	conserved hypothet	912	5	3.7	153	2	E90091	hypothetical prote
840	5	3.7	142	2	G72050	conserved hypothet	913	5	3.7	153	2	B83143	probable acetyltra
841	5	3.7	142	2	D86574	CR550 hypothetical	914	5	3.7	153	2	H72777	hypothetical prote
842	5	3.7	142	2	A87501	hypothetical prote	915	5	3.7	153	2	AG1363	hypothetical prote
843	5	3.7	142	2	A12479	hypothetical prote	916	5	3.7	154	1	D69425	conserved hypothet
844	5	3.7	142	2	B44355	CD44 glycoprotein	917	5	3.7	154	2	S72939	hypothetical prote
845	5	3.7	142	2	S46445	YMF46 protein - AC	918	5	3.7	154	2	G70724	hypothetical prote
846	5	3.7	142	2	AH1242	comG operon protei	919	5	3.7	154	2	T03503	conserved hypothet
847	5	3.7	143	2	S45537	peptidylprolyl iso	920	5	3.7	154	2	C93339	transcription regu
848	5	3.7	143	2	A69115	hypothetical prote	921	5	3.7	155	2	C83460	cytochrome C-type
849	5	3.7	143	2	F86168	hypothetical prote	922	5	3.7	155	2	H82879	ribosomal protein
850	5	3.7	143	2	T45347	hypothetical prote	923	5	3.7	155	2	S61835	cheW protein - Rhi
851	5	3.7	143	2	E70780	hypothetical prote	924	5	3.7	155	2	C75191	transcription regu
852	5	3.7	144	2	G86293	40S ribosomal prot	925	5	3.7	155	2	H84066	hypothetical prote
853	5	3.7	144	2	E84728	40S ribosomal prot	926	5	3.7	155	2	B97207	probable acetyltra
854	5	3.7	144	2	A83270	hypothetical prote	927	5	3.7	155	2	B71223	hypothetical prote
855	5	3.7	144	2	H81570	conserved hypothet	928	5	3.7	156	1	D43735	cellulose biosynth
856	5	3.7	144	2	A95285	hypothetical prote	929	5	3.7	156	2	PD0017	fertility restore
857	5	3.7	144	4	I51936	hypothetical BCR/A	930	5	3.7	156	2	E64084	kdtB protein - Hae
858	5	3.7	145	2	I39505	gene aac(6')-Ii pr	931	5	3.7	156	2	G69233	N-terminal acetyl
859	5	3.7	145	2	I39502	aminoglycoside 6'	932	5	3.7	156	2	AF2149	hypothetical prote
860	5	3.7	145	2	AG3271	LSU ribosomal prot	933	5	3.7	156	2	T32427	hypothetical prote
861	5	3.7	145	2	C83323	probable transcrip	934	5	3.7	156	2	A87366	hypothetical prote
862	5	3.7	145	2	F85690	hypothetical prote	935	5	3.7	156	2	D96706	unknown protein, 5
863	5	3.7	145	2	A70576	hypothetical prote	936	5	3.7	156	2	D70541	hypothetical prote
864	5	3.7	145	2	S30402	hypothetical prote	937	5	3.7	156	4	A24847	hypothetical BCR/A
865	5	3.7	145	2	AC0538	hypothetical prote	938	5	3.7	156	2	D72296	VP29-like phospho
866	5	3.7	145	2	AC2452	hypothetical prote	939	5	3.7	157	2	A53874	protein-tyrosine-p
867	5	3.7	145	2	B96705	unknown protein, 8	940	5	3.7	157	2	B53874	protein-tyrosine-p
868	5	3.7	145	2	E75490	hypothetical prote	941	5	3.7	157	2	E84220	molybdenum cofacto
869	5	3.7	145	2	A13048	transcription regu	942	5	3.7	157	2	AF0606	probable membrane
870	5	3.7	145	2	B98237	probable regulator	943	5	3.7	157	2	S58338	hypothetical prote
871	5	3.7	146	2	I39504	gene aac(6')-Ij pr	944	5	3.7	157	2	D72535	hypothetical prote
872	5	3.7	146	2	I39503	gene aac(6')-Ih pr	945	5	3.7	157	2	AH0939	probable membrane
873	5	3.7	146	2	S1810	trypsin inhibitor	946	5	3.7	157	2	AC1215	hypothetical prote
874	5	3.7	146	2	S51811	trypsin inhibitor	947	5	3.7	157	2	AG1568	hypothetical prote
875	5	3.7	146	2	S75815	hypothetical prote	948	5	3.7	158	2	S02758	retinoic acid rece
876	5	3.7	146	2	D95986	hypothetical prote	949	5	3.7	158	2	A71101	hypothetical prote
877	5	3.7	146	2	A95342	hypothetical prote	950	5	3.7	158	2	AI2899	conserved hypothet
878	5	3.7	146	2	AH1935	transcription regu	951	5	3.7	158	2	B17675	hypothetical prote
879	5	3.7	147	2	I51014	MHC class I protei	952	5	3.7	158	2	E87723	protein R06A10.3 [
880	5	3.7	147	2	D69008	conserved hypothet	953	5	3.7	158	2	B84588	probable AP2 domai
881	5	3.7	147	2	D71540	hypothetical prote	954	5	3.7	158	2	T00933	RNA-binding protei
882	5	3.7	147	2	T21719	hypothetical prote	955	5	3.7	158	2	G95925	probable acetyltra
883	5	3.7	147	2	H90305	hypothetical prote	956	5	3.7	159	2	AI1406	spermidine/spermin
884	5	3.7	147	2	D86389	hypothetical prote	957	5	3.7	159	2	AI1782	spermidine/spermin
885	5	3.7	148	2	B97768	hypothetical prote	958	5	3.7	159	2	AE2547	hypothetical prote
886	5	3.7	148	2	A39106	ribosomal protein	959	5	3.7	160	2	T32026	hypothetical prote
887	5	3.7	148	2	T03569	hypothetical 16.9K	960	5	3.7	160	2	S76609	hypothetical prote
888	5	3.7	148	2	A86538	CT053 hypothetical	961	5	3.7	160	2	B81322	peptidylprolyl iso
889	5	3.7	148	2	H72085	conserved hypothet	962	5	3.7	160	2	T29392	hypothetical prote
890	5	3.7	149	2	C87666	ribonuclease Hi [i	963	5	3.7	160	2	B95973	hypothetical expor
891	5	3.7	149	2	G72250	ribosomal protein	964	5	3.7	160	2	AB3559	transcription regu
892	5	3.7	149	2	T35846	probable integral	965	5	3.7	161	1	Z3BP79	gene 49.1 protein
893	5	3.7	149	2	E95201	hypothetical prote	966	5	3.7	161	2	A29557	calcium-binding pr
894	5	3.7	149	2	E98068	hypothetical prote	967	5	3.7	161	2	AC4921	calmodulin-like pr
895	5	3.7	149	2	H72746	hypothetical prote	968	5	3.7	161	2	A23597	bacterioferritin [
896	5	3.7	149	2	S53876	sex-regulated prot	969	5	3.7	161	2	S68771	bacterioferritin -
897	5	3.7	150	2	A54581	ribosomal protein	970	5	3.7	161	2	G64636	hypothetical prote
898	5	3.7	150	2	JS0024	15K calcium-bindin	971	5	3.7	161	2	D71879	hypothetical prote
899	5	3.7	150	2	A72328	conserved hypothet	972	5	3.7	161	2	A69181	hypothetical prote
900	5	3.7	150	2	D97188	uncharacterized pr	973	5	3.7	161	2	F72593	hypothetical prote
901	5	3.7	150	2	T36099	hypothetical prote	974	5	3.7	161	2	AC3085	conserved hypothet
902	5	3.7	150	2	G84173	archaeal histone A	975	5	3.7	161	2	E98221	hypothetical 23.2K
903	5	3.7	151	2	A69195	transcription regu	976	5	3.7	162	1	A53484	interleukin-15 pre
904	5	3.7	151	2	C48956	thioesterase - Art	977	5	3.7	162	1	TDMS	Thy-1 membrane gly
905	5	3.7	151	2	C84600	hypothetical prote	978	5	3.7	162	2	T50253	Vacuolar ATP synth

979 5 3.7 162 2 JG7157 calcium vector pro
980 5 3.7 162 2 A97591 cytochrome c-type
981 5 3.7 162 2 A82442 hypothetical prote
982 5 3.7 163 1 D69840 conserved hypothet
983 5 3.7 163 2 A72762 probable bacteriof
984 5 3.7 163 2 E69133 conserved hypothet
985 5 3.7 163 4 I39436 hypothetical BCR/A
986 5 3.7 164 2 H72231 ATP synthase F0, s
987 5 3.7 164 2 C84777 cyclophilin-like p
988 5 3.7 164 2 T29903 hypothetical prote
989 5 3.7 164 2 S52279 glutamate uptake r
990 5 3.7 164 2 JQ1252 hypothetical 16.7K
991 5 3.7 164 2 C70144 hypothetical prote
992 5 3.7 164 2 S35220 hypothetical prote
993 5 3.7 165 2 H84997 hypothetical prote
994 5 3.7 165 2 D81811 hypothetical prote
995 5 3.7 165 2 F82452 conserved hypothet
996 5 3.7 165 2 G30338 comG operon protei
997 5 3.7 165 2 A28138 interferon-induced
998 5 3.7 166 2 T45703 ubiquitin-protein
999 5 3.7 166 2 T43497 hypothetical prote
1000 5 3.7 166 2 A38122 ard protein - Bsch

ALIGNMENTS

RESULT 1
A69898 conserved hypothetical protein yozA - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: A69898
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
C: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadai, Y.; Satoh, T.; Scanlon,
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segkuchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69898
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-210 <KUN>
A:Cross-references: UNIPROT:O34947; GB:Z99114; GB:AL009126; NID:g2634230; PIDN:CAB13771
A:Experimental source: strain 168
C:Genetics:
A:Gene: yozA

Query Match 5.9%; Score 8; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 LANEGYLN 121
|||||
Db 116 LANEGYLN 123

RESULT 2
T36718 probable integral membrane protein - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T36718

R:Murphy, L.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, June 1999
A:Reference number: Z21612
A:Accession: T36718
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-253 <MUR>
A:Cross-references: UNIPROT:Q9XA15; EMBL:AL079308; PIDN:CAB45216.1; GSPDB:GN00070; SCOE
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOE8B:SCH69.19c

Query Match 5.2%; Score 7; DB 2; Length 253;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 65 LPETSKY 71
|||||
Db 188 LPETSKY 194

RESULT 3
C72418 hypothetical protein - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
C:Accession: C72418
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: C72418
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-257 <ARN>
A:Cross-references: UNIPROT:Q9WKV4; GB:AE001696; GB:AE000512; NID:g4980582; PIDN:AAD3519
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM0099
C:Superfamily: Thermotoga maritima hypothetical protein TM0099

Query Match 5.2%; Score 7; DB 2; Length 257;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 VFLELSA 63
|||||
Db 166 VFLELSA 172

RESULT 4
H75032 hypothetical protein PAB0826 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C:Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: H75032
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: H75032
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-285 <KAW>
A:Cross-references: UNIPROT:Q9UZA2; GB:AJ248287; GB:AL096836; NID:g5458657; PIDN:CAB5015
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB0826

Query Match 5.2%; Score 7; DB 2; Length 285;
Best Local Similarity 100.0%; Pred. No. 19;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 YLVSFVL 59
|||||

Db 25 YLVSFVL 31

RESULT 5

T27194
hypothetical protein Y57A10B.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T27194
R:Smyle, R.
submitted to the EMBL Data Library, October 1998
A:Reference number: Z20326
A:Accession: T27194
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-316 <WIL>
A:Cross-references: UNIPROT:Q9XWH8; EMBL:AL032647; PIDN:CAA21690.1; GSPDB:GN00019; CBSP:
A:Experimental source: clone Y57A10B
C:Genetics:
A:Gene: CESP:Y57A10B.3
A:Map position: 1
A:Introns: 54/2; 174/3; 226/1
C:Superfamily: Caenorhabditis elegans hypothetical protein K02E7.9

Query Match 5.2%; Score 7; DB 2; Length 316;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 SVFLELS 62
|||||

Db 295 SVFLELS 301

RESULT 6

AC3426
mannosyltransferase C (EC 2.4.1.-) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AC3426
R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mufier, C.; Los, T.; Ivanova,
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AC3426
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-377 <KUP>
A:Cross-references: UNIPROT:Q8YFW9; GB:AE008917; PIDN:AAL52574.1; PID:gl79833391; GSPDB:C
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI1393
A:Map position: 1
C:Keywords: glycosyltransferase; hexosyltransferase

Query Match 5.2%; Score 7; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 LELSAGL 65
|||||

Db 269 LELSAGL 275

RESULT 7

T35794
probable 4-aminobutyrate aminotransferase - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 09-Jul-2004

C:Accession: T35794
R:Murphy, L.; Harris, D.; Parkhill, J.; Barrall, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, August 1998
A:Reference number: Z21556
A:Accession: T35794
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-444 <MUR>
A:Cross-references: UNIPROT:O86823; EMBL:AL031225; PIDN:CAA20213.1; GSPDB:GN00070; SCOD:
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: gabT; SCODDB:SC8B7.02
C:Superfamily: ornithine-oxo-acid aminotransferase

Query Match 5.2%; Score 7; DB 2; Length 444;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 90 IREFASD 96
|||||

Db 245 IREFASD 251

RESULT 8

T48645
glycine betaine transport protein betL [validated] - Listeria monocytogenes
C:Species: Listeria monocytogenes
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C:Accession: T48645
R:Sleator, R.D.; Gahan, C.G.M.; Abbee, T.; Hill, C.
Appl. Environ. Microbiol. 65, 2078-2083, 1999
A:Title: Identification and disruption of betL, a secondary glycine betaine transport sy
A:Reference number: 224496; MUID:99240434; PMID:10224004
A:Accession: T48645
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-507 <SLE>
A:Cross-references: UNIPROT:Q9X4A5; EMBL:AF102174; NID:g4850173; PIDN:AAD30266.1; PID:g4
A:Experimental source: strain L028
C:Genetics:
A:Gene: betL
C:Function:
A:Description: responsible for glycine betaine uptake [validated, MUID:99240434]; seems
C:Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13
|||||

Db 415 DSATFVL 421

RESULT 9

AD1336
glycine betaine transporter BetL betL [imported] - Listeria monocytogenes (strain EGD-e)
C:Species: Listeria monocytogenes
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: AD1336
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AD1336
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-507 <GLA>
A:Cross-references: UNIPROT:Q9X4A5; GB:NC_003210; PIDN:CAD00170.1; PID:gl6411562; GSPDB:

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: betL

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 415 DSATFVL 421

RESULT 10

AB1707

glycine betaine transporter BetL [imported] - Listeria innocua (strain Clip11262)

C;Species: Listeria innocua

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AB1707

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, P.; Berche, P.; Bloeker

; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma

ok, C.; Schluecker, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AB1707

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-507 <GLA>

A;Cross-references: UNIPROT:Q929S7; GB:AU592022; PIDN:CAC97426.1; PID:gl6414710; GSPDB:G

A;Experimental source: strain Clip11262

C;Genetics:

A;Gene: betL

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 507;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 415 DSATFVL 421

RESULT 11

G69670

glycine betaine transporter opuD - Bacillus subtilis

C;Species: Bacillus subtilis

C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004

C;Accession: G69670

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte

C.; Bron, S.; Brouillet, S.; Bruchi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho

A.; Ehrlich, S.D.; Emerson, P.T.; Enian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galleg

lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Maunda, S.; Maue

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, C.M.; Portetelle

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A;Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seron

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K

A;Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69670

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-512 <KUN>

A;Cross-references: UNIPROT:P54417; GB:Z99119; GB:AL009126; NID:g2635411; PIDN:CAB14985.
A;Experimental source: strain 168

C;Genetics:

A;Gene: opuD

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 512;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 416 DSATFVL 422

RESULT 12

E89910

glycine betaine transporter opuD [imported] - Staphylococcus aureus (strain N315)

C;Species: Staphylococcus aureus

C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004

C;Accession: E89910

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;

C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A;Reference number: A89758; MUID:21311952; PMID:11418146

A;Accession: E89910

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-548 <KUR>

A;Cross-references: UNIPROT:Q99UC9; GB:BA000018; PID:gl3701146; PIDN:BA842441.1; GSPDB:G

A;Experimental source: strain N315

C;Genetics:

A;Gene: opuD

C;Superfamily: Escherichia coli probable carnitine transport protein

Query Match 5.2%; Score 7; DB 2; Length 548;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 DSATFVL 13

Db 423 DSATFVL 429

RESULT 13

C84534

hypothetical protein At2g15880 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: C84534

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; I

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: C84534

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-727 <STO>

A;Cross-references: UNIPROT:Q9XIL9; GB:AE002093; NID:g5306245; PIDN:AD41978.1; GSPDB:GN

A;Gene: At2g15880

A;Map position: 2

Query Match 5.2%; Score 7; DB 2; Length 727;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 PVYSPPL 31

Db 25 PVYSPPL 31

Db 665 PVSPPL 671

RESULT 14

F96586

hypotheical protein F20D21.29 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004

C:Accession: F96586

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.;

ansen, N.P.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: F96586

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-818 <STO>

A:Cross-references: UNIPROT:Q9SLI6; GB:AE005173; NID:G4585990; PIDN:AAD25626.1; GSPDB:GN

C:Genetics:

A:Gene: F20D21.29

A:Map position: 1

Query Match

5.2%; Score 7; DB 2; Length 818;

Best Local Similarity 100.0%; Pred.No. 47;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 59 LELSAGL 65

|||||

Db 111 LELSAGL 117

RESULT 15

T04377

probable pullulanase (EC 3.2.1.41) - barley

N:Alternate names: pullulanase

C:Species: Hordeum vulgare (barley)

C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004

C:Accession: T04377

R:Lok, F.; Kristensen, M.; Planchot, V.; Leah, R.; Svendsen, I.; Svenson, B.

submitted to the EMBL Data Library, December 1997

A:Description: Isolation and characterization of starch debranching enzyme, limit dextrin

A:Reference number: Z15320

A:Accession: T04377

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-904 <LOK>

A:Cross-references: UNIPROT:O48541; EMBL:AF022725; NID:G2502057; PIDN:AAD04189.1; PID:G2

A:Experimental source: cv. Igr1

C:Genetics:

A:Gene: HvLD99

A:Introns: 21/3; 70/1; 87/3; 124/1; 169/3; 235/2; 285/2; 305/3; 346/1; 376/2; 407/3; 439

C:Superfamily: pullulanase type debranching enzyme

C:Keywords: glycosidase; hydrolase

Query Match

5.2%; Score 7; DB 2; Length 904;

Best Local Similarity 100.0%; Pred.No. 52;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 62 SAGLPET 68

|||||

Db 81 SAGLPET 87

Search completed: July 20, 2005, 20:52:49

Job time : 20.2857 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:00 ; Search time 18.9571 Seconds
(without alignments)
673.517 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

Sequence: 1 SYMTINNFSCREEMGEVI.....EANGLLPDKLTLFCEVSVV 132

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : PIR 79:*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	30.3	409	2 S42384	Kruppel-like protein
2	7	5.3	136	1 B4956	flagellar protein
3	7	5.3	136	2 H9061	flagellar protein
4	7	5.3	136	2 H85809	hypothetical prote
5	7	5.3	143	2 A71051	hypothetical prote
6	7	5.3	145	2 F82133	hypothetical prote
7	7	5.3	296	2 J66050	homoserine kinase
8	7	5.3	296	2 H86769	homoserine kinase
9	7	5.3	302	2 H95075	hypothetical prote
10	7	5.3	304	2 D69744	conserved hypotet
11	7	5.3	310	2 C93088	hypothetical prote
12	7	5.3	311	2 A99196	purine nucleosidas
13	7	5.3	325	2 T45994	hypothetical prote
14	7	5.3	331	2 G75540	Elac family protei
15	7	5.3	340	2 G69474	conserved hypotet
16	7	5.3	401	2 E85253	hypothetical prote
17	7	5.3	421	2 I49734	HNF-3/foxa-head ho
18	7	5.3	441	2 B48854	hypothetical prote
19	7	5.3	563	1 C64420	N-methylhydantoina
20	7	5.3	567	2 J65538	Rab geranylgeranyl
21	7	5.3	567	2 A45977	Rab geranylgeranyl
22	7	5.3	583	1 A29576	H+/K+-exchanging A
23	7	5.3	660	2 H70798	probable cation-tr
24	7	5.3	684	2 E97943	Na+/H+ antiporter
25	7	5.3	745	1 B45995	copper-transportin
26	7	5.3	774	1 P3IV50	RNA-directed RNA p
27	7	5.3	774	2 S13670	basic polymerase 2
28	7	5.3	817	2 S77106	hypothetical prote
29	7	5.3	844	2 C86339	protein P2D10.12 [

30	7	5.3	1012	2 T42385	alpha-mannosidase
31	7	5.3	2160	2 T20241	hypothetical prote
32	7	5.3	3351	2 T13812	lipophorin - fruit
33	6	4.5	29	2 S51070	ribosomal protein
34	6	4.5	57	2 G98090	hypothetical prote
35	6	4.5	67	2 G71080	hypothetical prote
36	6	4.5	70	1 R5BPHK	regulatory protein
37	6	4.5	75	2 A54188	granulocyte chemot
38	6	4.5	75	2 S52630	nodulin ENOD40, ea
39	6	4.5	76	2 G82739	hypothetical prote
40	6	4.5	81	2 C21124	Bkm-like sex-deter
41	6	4.5	83	2 H71068	hypothetical prote
42	6	4.5	91	2 T30512	hypothetical prote
43	6	4.5	92	2 E82397	hypothetical prote
44	6	4.5	92	2 JN0095	hypothetical 10.6K
45	6	4.5	98	2 T11118	NADH2 dehydrogenas
46	6	4.5	99	2 S00210	plastocyanin b - L
47	6	4.5	106	2 H83754	multidrug resistanc
48	6	4.5	106	2 T24117	hypothetical prote
49	6	4.5	107	2 D97740	hypothetical prote
50	6	4.5	107	2 D71678	hypothetical prote
51	6	4.5	114	2 E75603	hypothetical prote
52	6	4.5	117	2 H72251	ribonuclease P pro
53	6	4.5	118	2 F72499	hypothetical prote
54	6	4.5	120	2 F71104	hypothetical prote
55	6	4.5	128	2 C83161	hypothetical prote
56	6	4.5	135	2 C72539	hypothetical prote
57	6	4.5	140	2 E81659	conserved hypotet
58	6	4.5	141	2 G71501	hypothetical prote
59	6	4.5	142	2 G72050	conserved hypotet
60	6	4.5	142	2 D86574	CT550 hypothetical
61	6	4.5	143	2 S19224	ribosomal protein
62	6	4.5	144	2 C95308	hypothetical prote
63	6	4.5	148	2 F71552	probable protein t
64	6	4.5	150	2 S44144	ribosomal protein
65	6	4.5	150	2 B70519	probable furA prot
66	6	4.5	154	2 B48230	T-cell receptor be
67	6	4.5	156	2 S37757	clathrin-associate
68	6	4.5	156	2 T47686	elicitor responsiv
69	6	4.5	157	2 D96689	calmodulin-related
70	6	4.5	157	2 S16728	polyferredoxin 2x2
71	6	4.5	165	2 S31618	T-cell receptor be
72	6	4.5	166	2 JN0030	early protein gp17
73	6	4.5	167	2 AD1978	hypothetical prote
74	6	4.5	168	1 CUPX	plastocyanin a pre
75	6	4.5	168	2 S58208	plastocyanin b pre
76	6	4.5	168	2 H90399	hypothetical prote
77	6	4.5	171	2 T41924	hypothetical prote
78	6	4.5	180	2 H86577	ribosome releasing
79	6	4.5	180	2 G72045	ribosome recycling
80	6	4.5	182	2 S65586	probable NDP-4-ket
81	6	4.5	184	2 AD1815	adenylate kinase [
82	6	4.5	184	2 F96691	probable 60S ribos
83	6	4.5	188	2 C90112	60S ribosomal prot
84	6	4.5	189	2 G96682	Flp13.3 [imported
85	6	4.5	189	2 AP1577	precorrin decarbox
86	6	4.5	191	2 S38117	hypothetical prote
87	6	4.5	193	2 E72641	hypothetical prote
88	6	4.5	195	2 G64359	adenylate kinase (
89	6	4.5	198	2 H95417	glutathione transf
90	6	4.5	201	2 H81925	hypothetical prote
91	6	4.5	201	2 A48236	hypothetical prote
92	6	4.5	202	1 JQ1556	transcription regu
93	6	4.5	202	2 C81181	coat protein - Bry
94	6	4.5	203	2 S64863	Maf/YceF/YhdE fami
95	6	4.5	205	2 S55670	probable membrane
96	6	4.5	210	2 A48226	hypothetical prote
97	6	4.5	210	2 H82670	ribosomal protein
98	6	4.5	214	1 JC4911	conserved hypotet
99	6	4.5	214	2 A42735	ribosomal protein
100	6	4.5	214	2 T20688	hypothetical prote
101	6	4.5	214	2 JC2013	ribosomal protein
102	6	4.5	214	2 B97143	hypothetical secre

103	6	4.5	216	2	S04207	sporamin B (clone	176	6	4.5	304	2	D70370	hypothetical prote
104	6	4.5	216	2	S07466	sporamin B precursor	177	6	4.5	305	2	A70482	ABC transporter -
105	6	4.5	216	2	A30835	sporamin precursor	178	6	4.5	307	2	D69521	hypothetical prote
106	6	4.5	218	2	S49596	ribosomal protein	179	6	4.5	308	2	I56573	synaptic glycoprot
107	6	4.5	219	2	S07465	sporamin A precursor	180	6	4.5	308	2	T50639	synaptic glycoprot
108	6	4.5	219	2	S04208	sporamin A (clone	181	6	4.5	308	2	T50638	synaptic glycoprot
109	6	4.5	219	2	E60110	repetitive protein	182	6	4.5	310	2	H90465	alcohol dehydrogen
110	6	4.5	219	2	E82825	hypothetical prote	183	6	4.5	313	2	D86219	protein P22013.19
111	6	4.5	220	2	E86277	hypothetical prote	184	6	4.5	313	2	D64089	survival protein s
112	6	4.5	220	2	T02068	probable transcrip	185	6	4.5	315	2	T46156	hypothetical prote
113	6	4.5	220	2	JQ2244	ribosomal protein	186	6	4.5	315	2	C81962	probable inner mem
114	6	4.5	220	2	A38575	gluconate 2-dehydr	187	6	4.5	316	2	T46000	hypothetical prote
115	6	4.5	220	2	S51444	hypothetical prote	188	6	4.5	318	1	F70536	3',5'-cyclic-nucle
116	6	4.5	221	2	A86396	60s ribosomal prot	189	6	4.5	318	2	F70822	hypothetical prote
117	6	4.5	221	1	C5NCM	peptidylprolyl iso	190	6	4.5	319	2	S73159	hypothetical prote
118	6	4.5	224	2	S49575	ribosomal protein	191	6	4.5	320	1	S20014	ubiquinol-cytochro
119	6	4.5	225	2	S57810	hypothetical prote	192	6	4.5	322	2	AC3207	conserved hypothet
120	6	4.5	225	2	T36733	probable transcrip	193	6	4.5	322	2	AG1929	hypothetical prote
121	6	4.5	226	1	LCRT	prolactin precursor	194	6	4.5	324	2	S28672	occr protein - Agr
122	6	4.5	228	2	T07957	probable ribosomal	195	6	4.5	324	2	F81018	iron(III) ABC tran
123	6	4.5	229	1	BVECHJ	molybdenum transpo	196	6	4.5	329	2	AG3055	succinoglycan bios
124	6	4.5	229	2	A00595	molybdenum transpo	197	6	4.5	332	2	C95150	SAP domain protein
125	6	4.5	229	2	H30727	molybdate transpor	198	6	4.5	334	2	T11633	hypothetical prote
126	6	4.5	229	2	A85579	molybdate transpor	199	6	4.5	334	2	E71706	hypothetical prote
127	6	4.5	231	2	AC2466	hypothetical prote	200	6	4.5	334	2	S48136	delichyl-phosphate
128	6	4.5	231	2	S05017	hypothetical prote	201	6	4.5	337	2	F98230	succinoglycan bios
129	6	4.5	232	2	G97109	response regulator	202	6	4.5	338	2	A96769	protein flavonol s
130	6	4.5	232	2	A35967	probable two compo	203	6	4.5	338	2	F84146	cytochrome d ubiq
131	6	4.5	233	2	C72105	conserved hypothet	204	6	4.5	339	2	G90311	acetoin catabolism
132	6	4.5	233	2	D86519	disulfide bond cha	205	6	4.5	341	2	AC3469	ABC transporter su
133	6	4.5	235	2	AC2170	hypothetical prote	206	6	4.5	345	2	G69138	conserved hypothet
134	6	4.5	238	1	S28674	hypothetical prote	207	6	4.5	348	2	S40750	hypothetical prote
135	6	4.5	238	2	D84827	probable protein k	208	6	4.5	353	2	S28548	protein kinase (EC
136	6	4.5	239	2	G84889	hypothetical prote	209	6	4.5	355	2	H95159	3-dehydroquinat s
137	6	4.5	239	2	S68257	phospholipase C (E	210	6	4.5	355	2	H98025	3-dehydroquinat s
138	6	4.5	241	2	D89928	hypothetical prote	211	6	4.5	356	2	C97010	hypothetical prote
139	6	4.5	242	2	F95256	hypothetical prote	212	6	4.5	356	2	T38408	conserved hypothet
140	6	4.5	242	2	G98121	ABC transporter, A	213	6	4.5	360	2	B90239	hypothetical prote
141	6	4.5	242	2	A75408	hypothetical prote	214	6	4.5	361	2	H96594	hypothetical prote
142	6	4.5	244	2	A75408	triophosphate is	215	6	4.5	362	1	JQ0735	recf protein - Pro
143	6	4.5	245	2	D97148	enoyl-CoA hydrat	216	6	4.5	366	2	T16249	hypothetical prote
144	6	4.5	246	2	E90309	hypothetical prote	217	6	4.5	367	2	T23387	hypothetical prote
145	6	4.5	250	2	C64304	ABC transporter su	218	6	4.5	367	2	A42937	probable transposa
146	6	4.5	251	2	B64337	hypothetical prote	219	6	4.5	368	2	E64142	hypothetical prote
147	6	4.5	253	2	JC5511	TATA-binding prote	220	6	4.5	368	2	G82870	Grp-binding protei
148	6	4.5	255	2	A81935	hypothetical prote	221	6	4.5	372	2	D81413	probable secreted
149	6	4.5	257	2	F88904	protein Y57G11C.3	222	6	4.5	372	2	S60207	fomF protein - Str
150	6	4.5	258	2	E90126	hypothetical prote	223	6	4.5	381	2	T28378	ORF MSV217 SCG gen
151	6	4.5	261	2	A00454	hypothetical prote	224	6	4.5	383	2	C90136	26S proteasome SU
152	6	4.5	261	2	H83848	cobalamin synthase	225	6	4.5	383	2	A96590	hypothetical prote
153	6	4.5	261	2	B83672	hypothetical prote	226	6	4.5	385	2	F75168	2-ketoglutarate fe
154	6	4.5	264	2	I39141	transcription fact	227	6	4.5	386	2	A96532	hypothetical prote
155	6	4.5	269	2	T27244	hypothetical prote	228	6	4.5	390	2	D83057	probable aminotran
156	6	4.5	269	2	B84429	hypothetical prote	229	6	4.5	390	2	AH2904	conserved hypothet
157	6	4.5	270	2	F86623	flagellar basal-bo	230	6	4.5	391	2	T34935	hypothetical prote
158	6	4.5	278	2	T37304	ras GTPase-activat	231	6	4.5	391	2	F82369	conserved hypothet
159	6	4.5	278	2	A47090	urease-associated	232	6	4.5	392	2	AD1485	ABC transporter, A
160	6	4.5	279	2	B70115	translational elong	233	6	4.5	393	2	AE3164	conserved hypothet
161	6	4.5	279	2	I64215	hypothetical prote	234	6	4.5	395	2	E97037	hypothetical prote
162	6	4.5	284	2	G70456	formyltetrahydrofo	235	6	4.5	396	1	TSEBBT	tryptophan synthas
163	6	4.5	284	2	S74352	phosphoribosylglyc	236	6	4.5	396	2	AF0268	tryptophan synthas
164	6	4.5	286	2	T02641	probable C2H2-type	237	6	4.5	396	2	S09627	prxR protein - Esc
165	6	4.5	290	2	D64335	nucleotide-binding	238	6	4.5	396	2	R83393	RND multidrug effl
166	6	4.5	291	2	T49260	hypothetical prote	239	6	4.5	396	2	T52445	hypothetical prote
167	6	4.5	294	2	T41953	G protein-coupled	240	6	4.5	396	2	S56954	protein YBR162c ho
168	6	4.5	295	2	H71306	probable cell divi	241	6	4.5	397	1	TSECB	tryptophan synthas
169	6	4.5	295	2	T00725	hypothetical prote	242	6	4.5	397	2	T47190	tryptophan synthas
170	6	4.5	295	2	F84456	hypothetical prote	243	6	4.5	397	2	AC0653	tryptophan synthas
171	6	4.5	298	2	H96584	hypothetical prote	244	6	4.5	397	2	G85761	tryptophan synthas
172	6	4.5	299	2	A39497	heterodisulfide re	245	6	4.5	397	2	A99858	tryptophan synthas
173	6	4.5	300	2	C69857	formyltetrahydrofo	246	6	4.5	398	2	H70393	hemolysin - Aquife
174	6	4.5	300	2	D83158	hypothetical prote	247	6	4.5	399	2	T32933	hypothetical prote
175	6	4.5	301	2	S73347	probable lipoprote	248	6	4.5	399	2	AC2785	MPS permease [drug

249	6	4.5	399	2	D97564	hypothetical prote	322	6	4.5	519	2	S36471	L2 protein - human
250	6	4.5	400	2	D28414	ORF MSV253 leucine	323	6	4.5	520	2	S36495	L2 cytochrome P450 4F
251	6	4.5	405	2	D75135	hypothetical prote	324	6	4.5	524	2	S29723	transcription fact
252	6	4.5	406	1	S48220	serine-type D-Ala-	325	6	4.5	524	2	S35551	probable ffh prote
253	6	4.5	407	2	S52148	amK protein - Erw	326	6	4.5	525	2	D70747	outer capsid prote
254	6	4.5	410	2	D83744	hypothetical prote	327	6	4.5	526	1	P5XR10	serine proteinase
255	6	4.5	410	2	T15442	hypothetical prote	328	6	4.5	530	2	F87590	hypothetical prote
256	6	4.5	414	2	A29835	SalI protein - Esc	329	6	4.5	530	2	F96491	F protein - Muraya
257	6	4.5	416	2	S75445	proteinase rhoB (E	330	6	4.5	534	2	A37483	serine-rich protei
258	6	4.5	419	2	D90025	molybdopterin bios	331	6	4.5	534	2	T39903	probable membrane
259	6	4.5	420	2	T42090	tryptophan synthas	332	6	4.5	535	2	S56261	hypothetical prote
260	6	4.5	423	2	I38056	nicotinic acetylch	333	6	4.5	540	2	C71260	transfer complex p
261	6	4.5	424	2	AF0350	histidine-tRNA lig	334	6	4.5	546	2	C56976	cytochrome-c oxida
262	6	4.5	424	2	B90083	gamma-tubulin [imp	335	6	4.5	549	1	D30010	oligopeptide ABC t
263	6	4.5	430	2	B84015	maltose/maltodextr	336	6	4.5	551	2	A11093	oligopeptide ABC t
264	6	4.5	430	2	S28707	hypothetical prote	337	6	4.5	551	2	AG1456	envelope protein -
265	6	4.5	436	2	G86009	probable cell-surf	338	6	4.5	551	2	TL3994	hybrid cluster [4F
266	6	4.5	439	2	T05134	hypothetical prote	339	6	4.5	553	1	S29861	exo-alpha-1,4-gluc
267	6	4.5	439	2	E70371	apolipoprotein N-a	340	6	4.5	553	2	D84133	hypothetical prote
268	6	4.5	441	2	T50436	hypothetical prote	341	6	4.5	553	2	F89960	hypothetical prote
269	6	4.5	444	1	D72631	probable IMP dehyd	342	6	4.5	554	2	H70011	exo-alpha-1,4-gluc
270	6	4.5	446	2	B97680	hypothetical prote	343	6	4.5	555	2	A43784	Xpo protein - Afri
271	6	4.5	447	2	F37828	conserved GTP-bind	344	6	4.5	559	2	A99237	hypothetical prote
272	6	4.5	447	2	H71673	hypothetical prote	345	6	4.5	560	2	S59859	rossetasome alpha
273	6	4.5	451	2	AG1141	hypothetical prote	346	6	4.5	565	2	T29718	hypothetical prote
274	6	4.5	451	2	AB1500	hypothetical prote	347	6	4.5	566	2	A86483	protein F5J5.13 [i
275	6	4.5	452	2	G90654	hypothetical prote	348	6	4.5	567	2	C64478	hypothetical prote
276	6	4.5	452	2	G85505	hypothetical prote	349	6	4.5	568	1	WZMCC	pectate lyase (EC
277	6	4.5	454	2	E84745	regulatory protein	350	6	4.5	568	2	S28792	pectate lyase (EC
278	6	4.5	454	2	T43069	probable serine pr	351	6	4.5	570	2	T04836	probable serine/th
279	6	4.5	455	2	C95049	acetyl-CoA carboxy	352	6	4.5	573	2	C86806	hypothetical prote
280	6	4.5	455	2	A97920	biotin carboxylase	353	6	4.5	575	2	S72283	DNA-directed RNA p
281	6	4.5	455	2	S51116	nicotinic acetylch	354	6	4.5	579	2	AF2094	hypothetical prote
282	6	4.5	455	2	A55972	nicotinic acetylch	355	6	4.5	580	2	T37664	hypothetical prote
283	6	4.5	461	2	AC0827	probable sensor ki	356	6	4.5	581	2	F97184	DNA modification m
284	6	4.5	462	2	S10439	nicotinic acetylch	357	6	4.5	582	1	ERADF2	fiber protein - hu
285	6	4.5	464	2	A33523	DNA-directed RNA p	358	6	4.5	585	2	T48513	hypothetical prote
286	6	4.5	467	2	AD2440	protechlorophyllid	359	6	4.5	586	2	JC7277	Sarcophaga-derived
287	6	4.5	467	2	A89899	heat shock protein	360	6	4.5	587	2	A84078	two-component sens
288	6	4.5	468	2	T49117	glucosidase like p	361	6	4.5	591	1	CBBY2	L-lactate dehydrog
289	6	4.5	468	2	T21331	hypothetical prote	362	6	4.5	593	2	C97848	ABC transporter Af
290	6	4.5	469	2	S74825	probable Rieske ir	363	6	4.5	594	2	T34855	probable glyoxylat
291	6	4.5	473	2	T04799	hypothetical prote	364	6	4.5	601	2	T51748	thimet oligopeptid
292	6	4.5	474	2	F97264	6-Phospho-Beta-D-G	365	6	4.5	608	2	T02684	MYB-related transc
293	6	4.5	476	2	AE0479	starch synthase (E	366	6	4.5	611	2	JE0365	alkylglycerone-pho
294	6	4.5	476	2	JC7189	tubulointerstitial	367	6	4.5	612	2	H81043	hypothetical prote
295	6	4.5	477	2	B69194	2-oxoacid-ferredox	368	6	4.5	622	2	S61140	probable membrane
296	6	4.5	480	2	G71050	asparagine synthas	369	6	4.5	622	2	B86309	Similar to mudra p
297	6	4.5	481	1	T43809	methylaspartate mu	370	6	4.5	627	2	C69637	DNA gyrase-like pr
298	6	4.5	481	2	B85575	probable glutamate	371	6	4.5	629	2	T19563	hypothetical prote
299	6	4.5	481	2	B90724	probable glutamate	372	6	4.5	635	2	T37239	serotonin receptor
300	6	4.5	482	2	S86945	protein fJL162c -	373	6	4.5	640	2	S67656	hypothetical prote
301	6	4.5	483	2	A90176	NADH dehydrogenase	374	6	4.5	644	2	B97885	transporter, trunc
302	6	4.5	487	2	C97144	probable membrane	375	6	4.5	644	2	B85758	RNase II, mRNA deg
303	6	4.5	488	2	T02207	protein 21D7 - com	376	6	4.5	644	2	A64877	exoribonuclease II
304	6	4.5	488	2	C72334	hypothetical prote	377	6	4.5	644	2	C90861	RNase II, mRNA deg
305	6	4.5	489	2	S77357	hypothetical prote	378	6	4.5	645	2	TL6078	hypothetical prote
306	6	4.5	492	2	F70326	conserved hypoteth	379	6	4.5	654	2	T29877	hypothetical prote
307	6	4.5	493	2	S49175	legumain (EC 3.4.2	380	6	4.5	656	2	S55262	UV-endonuclease -
308	6	4.5	496	2	F91056	probable 2-compone	381	6	4.5	657	2	T41546	hypothetical prote
309	6	4.5	496	2	B85901	probable 2-compone	382	6	4.5	669	2	D72423	iron(II) transport
310	6	4.5	496	2	C65033	Putative sensor-li	383	6	4.5	671	2	D86479	hypothetical prote
311	6	4.5	499	2	T18699	hypothetical prote	384	6	4.5	672	2	S63043	MET4 protein - yea
312	6	4.5	499	2	T47722	probable protein k	385	6	4.5	682	2	B84021	two-component sens
313	6	4.5	500	2	D90395	conserved hypoteth	386	6	4.5	683	2	T37240	serotonin receptor
314	6	4.5	501	2	D86815	xylokinase (EC 2	387	6	4.5	690	2	I51298	transforming prote
315	6	4.5	502	2	AG3641	histidine-tRNA lig	388	6	4.5	690	2	S62728	transposase - phag
316	6	4.5	505	2	S39962	endoglucanase - Er	389	6	4.5	691	2	A40024	regulatory protein
317	6	4.5	516	2	E86062	probable 2-compone	390	6	4.5	694	2	T01504	hypothetical prote
318	6	4.5	516	2	D91216	probable 2-compone	391	6	4.5	697	2	T37946	tryptophan synthas
319	6	4.5	516	2	J00872	hypothetical 56.2K	392	6	4.5	699	2	T14904	NADPH-ferrihemopro
320	6	4.5	516	2	F97541	methionyl-tRNA syn	393	6	4.5	699	2	A43734	probable protein k
321	6	4.5	516	2	AH2760	methionyl-tRNA syn	394	6	4.5	728	2	S43768	transcription acti

395	729	2	D72079	conserved hypother	468	6	4.5	1466	2	Tl17138
396	729	2	H86544	Cr283 hypotherical	469	6	4.5	1467	2	Tl18411
397	730	2	T42937	hypotherical prote	470	6	4.5	1471	2	Tl17149
398	731	2	D36808	hypotherical prote	471	6	4.5	1472	2	Tl18413
399	743	2	D84545	probable salt-indu	472	6	4.5	1501	2	S50992
400	743	2	C56695	transducin-like en	473	6	4.5	1510	2	Tl17145
401	744	2	T13485	NADH2 dehydrognas	474	6	4.5	1515	2	Tl17156
402	744	2	G90124	hypotherical prote	475	6	4.5	1581	2	T32963
403	747	2	F88561	protein F58A4.11 I	476	6	4.5	1649	2	T39938
404	761	2	S20458	pqqF protein - Kle	477	6	4.5	1683	2	S56811
405	765	2	H84247	adaptive-response	478	6	4.5	1706	2	I84499
406	776	2	T24262	hypotherical prote	479	6	4.5	1711	2	T21432
407	778	2	JC7797	scallop unconventi	480	6	4.5	1780	2	Tl17272
408	779	2	A57177	NIMA-like protein	481	6	4.5	1822	2	T14106
409	790	2	T19040	hypotherical prote	482	6	4.5	1868	2	T32707
410	795	2	D64343	hypotherical prote	483	6	4.5	1879	2	Tl19481
411	798	2	T41616	hypotherical prote	484	6	4.5	1921	2	Tl13827
412	805	2	AH2731	ATP-dependent prot	485	6	4.5	2026	1	OYBY
413	805	2	G97512	ATP-dependent prot	486	6	4.5	2030	2	T33162
414	809	2	F81312	leucine-tRNA ligas	487	6	4.5	2161	1	A45389
415	811	2	B82365	glycerol-3-phospha	488	6	4.5	2231	2	D71870
416	811	2	T08738	hypotherical prote	489	6	4.5	2523	2	F70846
417	819	2	T19351	hypotherical prote	490	6	4.5	2657	2	Tl8497
418	832	2	T49494	condensin complex	491	6	4.5	2761	2	T29285
419	835	2	Tl15177	hypotherical prote	492	6	4.5	2774	2	A43359
420	839	2	D86260	protein Tl2C24.24	493	6	4.5	2960	2	A45259
421	840	2	E96541	unknown protein [i	494	6	4.5	3972	2	S75251
422	845	2	D86301	F19K19.8 protein -	495	6	4.5	4199	2	S76412
423	853	2	D95365	NADH2 dehydrognas	496	6	4.5	4342	2	H83343
424	891	2	B82495	probable NADH dehy	497	6	4.5	4644	1	A38905
425	935	2	S66306	hypotherical prote	498	5	3.8	10	2	A31571
426	942	2	B72015	metalloproteinase,	499	5	3.8	11	2	PH0903
427	942	2	C86610	insulinase family//	500	5	3.8	13	2	E53275
428	954	2	I51703	c-kit-related.kina	501	5	3.8	14	2	I64815
429	956	2	Tl9046	ras GTPase-activat	502	5	3.8	17	2	B42576
430	958	2	E81701	alpha-amylase G-6	503	5	3.8	17	2	A46218
431	967	2	Tl5680	hypotherical prote	504	5	3.8	20	2	A56045
432	993	2	D96812	protein F3P9.12 [i	505	5	3.8	21	2	I58423
433	1003	2	A39521	glycine dehydrogen	506	5	3.8	24	2	A43503
434	1003	2	Tl13856	ksr protein - frui	507	5	3.8	27	2	I50388
435	1018	1	GNWKG7	genome polyprote-in	508	5	3.8	27	2	H64520
436	1039	2	A85096	hypotherical prote	509	5	3.8	27	2	A05058
437	1048	2	T13045	ras GTPase-activat	510	5	3.8	30	2	E84786
438	1051	2	S27002	phospholipase C (E	511	5	3.8	31	2	S53289
439	1057	2	S09112	hypotherical prote	512	5	3.8	31	2	I48082
440	1093	2	A47212	transcription fact	513	5	3.8	36	2	T22102
441	1128	2	T30296	R27-2 protein - ir	514	5	3.8	39	2	AB0930
442	1137	2	D89610	ras GTPase-activat	515	5	3.8	39	2	AF0836
443	1141	2	T29104	Tbcl protein - mou	516	5	3.8	39	2	F82226
444	1146	2	F84487	probable ABC trans	517	5	3.8	39	2	C97037
445	1165	2	A48667	peroxisomal assemb	518	5	3.8	40	2	C32338
446	1170	2	Tl9042	ras GTPase-activat	519	5	3.8	47	2	D97948
447	1186	2	A81294	pyruvate-flavodoxi	520	5	3.8	49	2	F82255
448	1189	2	S56852	hypotherical prote	521	5	3.8	51	2	I57670
449	1196	2	S65245	translation elonga	522	5	3.8	51	2	C81117
450	1207	2	T70013	conserved hypother	523	5	3.8	51	2	C82658
451	1207	2	Tl9041	ras GTPase-activat	524	5	3.8	51	2	AI1731
452	1217	2	A45493	phospholipase C-be	525	5	3.8	52	2	G97873
453	1219	2	Tl4578	nucleoporin Nup153	526	5	3.8	53	2	S10355
454	1220	1	DJBEC3	DNA-directed DNA p	527	5	3.8	53	2	H98038
455	1220	2	T42573	DNA-directed DNA p	528	5	3.8	54	2	D26506
456	1224	2	T25770	hypotherical prote	529	5	3.8	54	2	A90543
457	1234	2	S52099	phospholipase C be	530	5	3.8	54	2	T42318
458	1234	2	I38994	phospholipase C-be	531	5	3.8	54	2	H82199
459	1253	1	A44400	myosin heavy chain	532	5	3.8	55	2	E70593
460	1259	2	Tl9043	ras GTPase-activat	533	5	3.8	55	2	Tl1184
461	1270	2	T22615	hypotherical prote	534	5	3.8	55	2	D95140
462	1302	2	T23236	hypotherical prote	535	5	3.8	55	2	T25692
463	1325	2	T01037	hypotherical prote	536	5	3.8	56	2	I53423
464	1336	2	Tl8288	ABC transport prot	537	5	3.8	56	2	S36812
465	1337	1	I38670	protein-tyrosine-p	538	5	3.8	56	2	G72592
466	1392	2	A43336	microtubule-vesicl	539	5	3.8	57	2	G97910
467	1427	2	S22695	restin - human	540	5	3.8	57	2	AH0423

541	3.8	58	2	S31551	ribulose-bisphosph	614	5	3.8	89	2	T08479	plasmid maintenanc
542	3.8	58	2	T13185	hypothetical prote	615	5	3.8	89	2	F82757	hypothetical prote
543	3.8	59	2	H91210	hypothetical prote	616	5	3.8	89	2	AH2653	hypothetical prote
544	3.8	59	2	F98276	hypothetical prote	617	5	3.8	90	2	C81917	hypothetical prote
545	3.8	60	2	I55550	low density lipopr	618	5	3.8	90	2	A81186	hypothetical prote
546	3.8	61	2	A21444	hypothetical prote	619	5	3.8	90	2	AB1207	B. subtilis Ykta p
547	3.8	63	2	A56886	natural killer enh	620	5	3.8	90	2	AI1563	B. subtilis Ykta p
548	3.8	63	2	T28361	ORF MSV200 hypothe	621	5	3.8	91	1	W5WL11	ESA protein - huma
549	3.8	65	2	E83492	hypothetical prote	622	5	3.8	91	1	W5WL6A	ESA protein - huma
550	3.8	67	2	C47036	archaeal histone H	623	5	3.8	91	2	B61055	ESA protein - huma
551	3.8	68	2	E69437	conserved hypothet	624	5	3.8	91	2	T24120	hypothetical prote
552	3.8	68	2	G69209	histone-related pr	625	5	3.8	91	2	E97841	hypothetical prote
553	3.8	69	2	S60826	M protein precursor	626	5	3.8	91	2	AC3075	sarcosine oxidase
554	3.8	69	2	A47036	histone-related pr	627	5	3.8	91	2	F98211	sarcosine oxidase
555	3.8	69	2	T48848	histone Hmf1 [lmpo	628	5	3.8	92	2	FV0007	hypothetical prote
556	3.8	70	2	S76907	hypothetical prote	629	5	3.8	92	2	F90898	probable tail fibe
557	3.8	70	2	B64863	hypothetical prote	630	5	3.8	92	2	T14937	hypothetical prote
558	3.8	71	2	H64454	hypothetical prote	631	5	3.8	92	2	A85842	hypothetical prote
559	3.8	71	2	AG2418	hypothetical prote	632	5	3.8	93	2	A99311	small subunit of i
560	3.8	72	2	S30987	gene 42 protein -	633	5	3.8	93	2	D97144	hypothetical prote
561	3.8	72	2	T26975	hypothetical prote	634	5	3.8	93	2	D97144	hypothetical prote
562	3.8	72	2	AD0096	probable membrane	635	5	3.8	94	1	W5WLC1	E5 protein - pygmy
563	3.8	73	2	C97172	carbon storage reg	636	5	3.8	94	2	I48172	glial fibrillary a
564	3.8	74	2	T31047	hypothetical prote	637	5	3.8	94	2	A41492	lik heat shock pro
565	3.8	75	2	AD0882	probable membrane	638	5	3.8	94	2	F97064	spore coat protein
566	3.8	75	2	D61399	hypothetical prote	639	5	3.8	95	2	S66015	ribosomal protein
567	3.8	77	1	C58652	adipokinetic hormo	640	5	3.8	95	2	D84327	hypothetical prote
568	3.8	77	2	D82819	hypothetical prote	641	5	3.8	95	2	AD0981	conserved hypothet
569	3.8	77	2	S1867	ubiquitin-like pro	642	5	3.8	95	2	B82131	conserved hypothet
570	3.8	78	2	P00053	hypothetical prote	643	5	3.8	95	2	H69767	hypothetical prote
571	3.8	78	2	C83319	conserved hypothet	644	5	3.8	96	2	I68741	integral membrane
572	3.8	78	2	T33454	hypothetical prote	645	5	3.8	96	2	AE2331	50S ribosomal prot
573	3.8	78	2	S75256	tyrosine-tRNA liga	646	5	3.8	96	2	G81019	chaperonin, 10 kDa
574	3.8	79	1	A58656	adipokinetic hormo	647	5	3.8	96	2	G81964	chaperonin 10 kD s
575	3.8	79	2	S03266	aspartic proteinas	648	5	3.8	96	2	E69110	hypothetical prote
576	3.8	79	2	R83671	hypothetical prote	649	5	3.8	96	2	C64900	outer membrane por
577	3.8	79	2	E37204	uncharacterized Zn	650	5	3.8	97	2	AI0538	hypothetical prote
578	3.8	80	2	S21770	saposin-C - bovine	651	5	3.8	97	2	T25754	hypothetical prote
579	3.8	80	2	G64030	hypothetical prote	652	5	3.8	98	2	A99613	NADH dehydrogenase
580	3.8	80	2	T49980	hypothetical prote	653	5	3.8	98	2	T11527	NADH2 dehydrogenas
581	3.8	80	2	T48081	hypothetical prote	654	5	3.8	98	2	T11135	NADH2 dehydrogenas
582	3.8	81	2	T38451	probable glycoprot	655	5	3.8	98	2	T12887	hypothetical prote
583	3.8	81	2	D97617	hypothetical prote	656	5	3.8	99	2	S03525	t-cell receptor al
584	3.8	82	2	AB0009	glutaredoxin [lmpo	657	5	3.8	99	2	E83235	hypothetical prote
585	3.8	83	2	A70768	hypothetical prote	658	5	3.8	99	2	C48653	hypothetical prote
586	3.8	83	2	D69153	hypothetical prote	659	5	3.8	100	2	S50333	NADH2 dehydrogenas
587	3.8	83	2	T48068	hypothetical prote	660	5	3.8	100	2	S29559	conserved hypothet
588	3.8	83	2	AD1082	B. subtilis Ykud p	661	5	3.8	100	2	AH0077	spore coat peptide
589	3.8	83	2	AE1439	B. subtilis Ykud p	662	5	3.8	100	2	G69605	spore coat peptide
590	3.8	83	2	AP2544	thioredoxin asl764	663	5	3.8	100	2	F87191	hypothetical prote
591	3.8	84	2	AC0027	30S ribosomal prot	664	5	3.8	100	2	T23389	hypothetical prote
592	3.8	84	2	T10348	hypothetical prote	665	5	3.8	100	2	C97492	hypothetical prote
593	3.8	84	2	E72859	AcOrf-76 protein -	666	5	3.8	100	2	AB2710	conserved hypothet
594	3.8	84	2	S36691	hypothetical prote	667	5	3.8	100	2	B98008	hypothetical prote
595	3.8	85	1	E64093	ribosomal protein	668	5	3.8	101	2	AC2905	4a-hydroxytetrahyd
596	3.8	85	2	A61616	depressant insect	669	5	3.8	101	2	E37476	E4 orf 3' of fiber
597	3.8	85	2	I40691	immunity protein 8	670	5	3.8	101	2	E82484	hypothetical prote
598	3.8	85	2	T41819	AcWNPV orf76 - Bom	671	5	3.8	101	2	C83047	conserved hypothet
599	3.8	86	2	H71510	probable swib (ym7	672	5	3.8	101	2	T25656	hypothetical prote
600	3.8	86	2	AB1669	conserved hypothet	673	5	3.8	101	2	AC3161	DNA-invertase [lmp
601	3.8	87	1	R3NT15	ribosomal protein	674	5	3.8	102	2	E34770	ORF2 protein - sai
602	3.8	87	2	E69071	hypothetical prote	675	5	3.8	102	2	F69475	conserved hypothet
603	3.8	88	1	R3YML9	ribosomal protein	676	5	3.8	102	2	S65294	probable membrane
604	3.8	88	2	S08815	M protein precursor	677	5	3.8	102	2	D72757	hypothetical prote
605	3.8	88	2	S68163	SH2 protein - yea	678	5	3.8	103	2	I50417	RSV-induced protei
606	3.8	88	2	AC2561	hypothetical prote	679	5	3.8	103	2	A26736	transformation-ind
607	3.8	89	1	S42609	shiga-like toxin -	680	5	3.8	103	2	T49368	hypothetical prote
608	3.8	89	2	S58344	shiga-like toxin I	681	5	3.8	103	2	H90234	hypothetical prote
609	3.8	89	2	F90779	Shiga toxin 2 subu	682	5	3.8	103	2	S59561	nucleosome assembl
610	3.8	89	2	H85640	Shiga toxin 2 subu	683	5	3.8	103	2	D71047	hypothetical prote
611	3.8	89	2	AG0279	shiga-like toxin I	684	5	3.8	104	2	I47165	cyclolytic trigger
612	3.8	89	2	I69156	shiga-like toxin I	685	5	3.8	104	2	E69805	hypothetical prote
613	3.8	89	2	S01033	shiga-like toxin I	686	5	3.8	104	2	T49766	hypothetical prote

687	5	3.8	105	2	S36396	H+-transporting tw	760	5	3.8	117	2	Tl3187	hypothetical prote
688	5	3.8	105	2	Tl0473	molt-inhibiting ho	761	5	3.8	117	2	T35913	hypothetical prote
689	5	3.8	105	2	D69619	multidrug resistanc	762	5	3.8	117	2	Tl4283	embryogenic callus
690	5	3.8	105	2	S07742	hypothetical prote	763	5	3.8	117	2	F72468	hypothetical prote
691	5	3.8	105	2	Tl7281	hypothetical prote	764	-5	3.8	118	2	S21918	T-cell receptor al
692	5	3.8	106	2	C97043	hypothetical prote	765	5	3.8	118	2	S27187	multidrug resistanc
693	5	3.8	107	2	D84391	hypothetical prote	766	5	3.8	118	2	S76608	hypothetical prote
694	5	3.8	107	2	S78532	MCP-1 protein spl	767	5	3.8	118	2	T07177	probable oleoyl-la
695	5	3.8	107	2	C81420	hypothetical prote	768	5	3.8	118	2	D75065	hypothetical prote
696	5	3.8	107	2	A82642	conserved plasmin	769	5	3.8	118	2	D75065	hypothetical prote
697	5	3.8	107	2	S23472	cpcF protein - Fis	770	5	3.8	118	2	F90459	hypothetical prote
698	5	3.8	107	2	D72487	hypothetical prote	771	5	3.8	118	2	Tl6510	hypothetical prote
699	5	3.8	107	2	B72494	hypothetical prote	772	5	3.8	118	4	S62173	hypothetical prote
700	5	3.8	108	2	AD1714	thioredoxin homolo	773	5	3.8	119	2	A43635	nitrogenase (EC 1.
701	5	3.8	108	2	AD1343	thioredoxin homolo	774	5	3.8	119	2	AB0043	probable cation to
702	5	3.8	108	2	T04117	SEC18 protein homo	775	5	3.8	119	2	S55161	hypothetical prote
703	5	3.8	108	2	T26539	hypothetical prote	776	5	3.8	119	2	H70476	hypothetical prote
704	5	3.8	108	2	B81285	hypothetical prote	777	5	3.8	119	2	A11138	hypothetical prote
705	5	3.8	108	2	C64455	hypothetical prote	778	5	3.8	119	2	C84504	probable CCHC-type
706	5	3.8	108	2	A00116	conserved hypothet	779	5	3.8	119	2	G69112	hypothetical prote
707	5	3.8	108	2	T21447	hypothetical prote	780	5	3.8	119	2	AC1227	hypothetical prote
708	5	3.8	109	1	T7HUSE	transforming prote	781	5	3.8	119	2	A86271	F21F23.19 protein
709	5	3.8	109	2	S27053	thioredoxin - 3mer	782	5	3.8	119	2	A71167	hypothetical prote
710	5	3.8	109	2	T36708	hypothetical prote	783	5	3.8	120	2	C64358	ribosomal protein
711	5	3.8	109	2	S41018	hypothetical prote	784	5	3.8	120	2	F97537	probable glycine c
712	5	3.8	109	2	C72685	hypothetical prote	785	5	3.8	120	2	AG2756	glycine cleavage s
713	5	3.8	109	2	A96757	hypothetical prote	786	5	3.8	120	2	AC0632	membrane protein,
714	5	3.8	109	2	C95914	hypothetical hame-	787	5	3.8	120	2	A70799	probable transcrip
715	5	3.8	109	2	D87449	conserved hypothet	788	5	3.8	120	2	JC2475	growth hormone reg
716	5	3.8	109	2	T46171	hypothetical prote	789	5	3.8	121	2	S11671	hypothetical prote
717	5	3.8	110	1	RSBYA1	acidic ribosomal p	790	5	3.8	121	2	B36858	GLI protein - vari
718	5	3.8	110	1	R5RTA	ribosomal protein	791	5	3.8	121	2	Tl8126	hypothetical prote
719	5	3.8	110	1	R5XL32	ribosomal protein	792	5	3.8	121	2	T40222	hypothetical prote
720	5	3.8	110	2	C71076	hypothetical prote	793	5	3.8	122	2	AG2613	conserved hypothet
721	5	3.8	110	2	E71083	hypothetical prote	794	5	3.8	122	2	E97395	hypothetical prote
722	5	3.8	110	2	D82502	hypothetical prote	795	5	3.8	122	2	S57090	hypothetical prote
723	5	3.8	110	2	A38529	nika protein - Esc	796	5	3.8	122	2	AB0895	probable exported
724	5	3.8	110	2	A11860	hypothetical prote	797	5	3.8	122	2	A83756	hypothetical prote
725	5	3.8	111	2	S22899	T-cell receptor al	798	5	3.8	122	2	E90948	hypothetical prote
726	5	3.8	111	2	AG1906	photosystem II pro	799	5	3.8	122	2	G64946	lipoprotein yebf p
727	5	3.8	111	2	T72501	hypothetical prote	800	5	3.8	122	2	A85797	hypothetical prote
728	5	3.8	111	2	T49768	hypothetical prote	801	5	3.8	122	2	F69347	hypothetical prote
729	5	3.8	111	2	T19357	hypothetical prote	802	5	3.8	123	2	S64248	hypothetical prote
730	5	3.8	111	2	AB3120	ferredoxin [import	803	5	3.8	123	2	B82502	phage shock protei
731	5	3.8	112	2	E86205	hypothetical prote	804	5	3.8	124	1	T34207	ribosomal protein
732	5	3.8	112	2	B96771	protein ribosomal	805	5	3.8	124	2	S57715	chitinase (EC 3.2.
733	5	3.8	112	2	S73994	hypothetical prote	806	5	3.8	124	2	B70101	holo-acyl-carrier
734	5	3.8	112	2	T15328	hypothetical prote	807	5	3.8	124	2	F95150	crCB protein [impo
735	5	3.8	112	2	B95380	hypothetical prote	808	5	3.8	124	2	D98018	crCB protein [impo
736	5	3.8	113	2	A41830	hypothetical prote	809	5	3.8	124	2	E90804	probable structural
737	5	3.8	113	2	S66967	probable membrane	810	5	3.8	124	2	A85613	hypothetical prote
738	5	3.8	113	2	T48774	hypothetical prote	811	5	3.8	124	2	S08640	hypothetical prote
739	5	3.8	113	2	B41657	probable immunity	812	5	3.8	124	2	T45917	hypothetical prote
740	5	3.8	113	2	C83893	procylic acid r	813	5	3.8	124	2	T34150	hypothetical prote
741	5	3.8	114	2	A30229	procylic acid r	814	5	3.8	124	2	A72464	hypothetical prote
742	5	3.8	114	2	T38286	T cell leukemia/ly	815	5	3.8	124	2	F97745	hypothetical prote
743	5	3.8	114	2	F71925	cag island protein	816	5	3.8	125	2	C83599	conserved hypothet
744	5	3.8	114	2	H64586	cag pathogenicity	817	5	3.8	125	2	A87402	conserved hypothet
745	5	3.8	114	2	C90324	hypothetical prote	818	5	3.8	125	2	D97435	hypothetical prote
746	5	3.8	115	1	FAUTPC	procylic acid r	819	5	3.8	126	2	B69989	hypothetical prote
747	5	3.8	115	2	S78279	photosystem II pro	820	5	3.8	126	2	C69776	hypothetical prote
748	5	3.8	115	2	G71058	hypothetical prote	821	5	3.8	126	2	AB2905	conserved hypothet
749	5	3.8	115	2	H72583	hypothetical prote	822	5	3.8	126	2	F83536	probable ring-clea
750	5	3.8	115	2	AE2185	hypothetical prote	823	5	3.8	127	2	A58933	ribosomal protein
751	5	3.8	115	2	D75434	hypothetical prote	824	5	3.8	127	2	S09372	hypothetical prote
752	5	3.8	115	2	AF1366	transcription regu	825	5	3.8	127	2	T43781	hypothetical prote
753	5	3.8	115	2	AG1735	transcription regu	826	5	3.8	127	2	F65098	hypothetical prote
754	5	3.8	115	2	E98167	ferredoxin II (AF2	827	5	3.8	127	2	C91126	hypothetical 14.5
755	5	3.8	116	2	S07258	helix-destabilizin	828	5	3.8	127	2	H85971	hypothetical prote
756	5	3.8	116	2	D71454	hypothetical prote	829	5	3.8	128	2	S57955	thrombospondin 2 -
757	5	3.8	116	2	C72549	hypothetical prote	830	5	3.8	128	2	F67956	hypothetical prote
758	5	3.8	116	2	B99304	hypothetical prote	831	5	3.8	128	2	A70112	hypothetical prote
759	5	3.8	117	2	G71190	hypothetical prote	832	5	3.8	128	2	S53584	probable membrane

833 128 2 AF1998 hypothetical prote
834 129 2 S59126 histone H2A (clone
835 129 2 A26036 procyclic acidic r
836 129 2 G90528 hypothetical prote
837 129 2 H87659 conserved hypothet
838 129 2 F64117 embryonic abundant
839 129 2 G70667 hypothetical prote
840 129 2 D82627 hypothetical prote
841 130 1 Q7BP77 gene 7.7 protein -
842 130 2 A88579 protein T07C4.5 [i
843 130 2 S72926 hypothetical prote
844 130 2 T10347 hypothetical prote
845 130 2 T27438 hypothetical prote
846 130 2 S14983 extensin class I (
847 130 2 G35905 hypothetical prote
848 130 2 G72594 hypothetical prote
849 131 2 H86382 hypothetical prote
850 131 2 F69103 hypothetical prote
851 131 2 F75117 hypothetical prote
852 132 1 E70434 conserved hypothet
853 132 2 A44864 fatty acid-binding
854 132 2 T29160 hypothetical prote
855 132 2 F42512 G-ORF-A protein -
856 132 2 D82278 hypothetical prote
857 132 2 D83003 hypothetical prote
858 132 2 E72603 hypothetical prote
859 132 2 T30595 sugar transport ho
860 133 1 R3FF49 ribosomal protein
861 133 2 S77948 major allergen Par
862 133 2 A75314 ribosomal protein
863 133 2 T14810 ribosomal protein -
864 133 2 S70967 bfpG protein - Bsc
865 133 2 H75296 hypothetical prote
866 133 2 T07205 hypothetical prote
867 133 2 A82955 hypothetical prote
868 133 2 D97680 hypothetical prote
869 133 2 A89917 hypothetical prote
870 133 2 E70334 hypothetical prote
871 133 2 AF2561 hypothetical prote
872 134 1 R3FF32 ribosomal protein
873 134 2 A00326 probable membrane
874 134 2 A72754 hypothetical prote
875 134 2 F75170 hypothetical prote
876 134 2 F69182 conserved hypothet
877 134 2 C82030 probable cytochrom
878 135 1 RSHU32 ribosomal protein
879 135 1 RSM332 ribosomal protein
880 135 1 R5RT32 ribosomal protein
881 135 2 I58276 ribosomal protein
882 135 2 S41979 nuclease inhibitor
883 135 2 A12522 sugar-non-specific
884 135 2 E75616 hypothetical prote
885 135 2 H82834 hypothetical prote
886 135 2 C90527 hypothetical prote
887 135 2 A10541 probable secreted
888 135 2 B44438 gene ldmr1 protei
889 136 2 G84248 hypothetical prote
890 136 2 S19479 hypothetical prote
891 136 2 B75086 hypothetical prote
892 136 2 E37847 hypothetical prote
893 137 2 S43885 3-isopropylmalate
894 137 2 D86944 conserved hypothet
895 138 1 R5FM29 ribosomal protein
896 138 2 S52933 major allergen Par
897 138 2 PC2224 peptide LIAE 2 - p
898 138 2 S73943 MG076 homolog G07
899 138 2 E84329 hypothetical prote
900 138 2 B87594 proteinase, probab
901 138 2 A96039 degenerate transpo
902 139 2 T11639 ribosomal protein
903 139 2 AG2743 dnak deletion supp
904 139 2 T25974 hypothetical prote
905 140 1 SXAD92 hexon-associated p

906 140 1 SXAD95
907 140 2 T03693 ribosomal protein
908 140 2 F84744 60S ribosomal prot
909 140 2 AH1517 hypothetical prote
910 140 2 T49347 hypothetical prote
911 140 2 E86283 hypothetical prote
912 140 2 I38232 gene SMA3 protein
913 140 2 I38233 gene SMA4 protein
914 140 2 I38234 gene SMA5 protein
915 141 2 A44438 multidrug drug res
916 141 2 S25272 gene V protein - p
917 141 2 B70916 hypothetical prote
918 141 2 JQ1669 hypothetical prote
919 141 2 A90130 hypothetical prote
920 141 2 S42721 interlukin-3 prec
921 142 1 S42722 interlukin-3 prec
922 142 2 E90134 40S ribosomal prot
923 142 2 E84040 hypothetical prote
924 142 2 F90015 galactose-6-phosph
925 142 2 A38158 galactose-6-phosph
926 142 2 JQ2280 low-temperature re
927 142 2 T51902 hypothetical prote
928 142 2 S70484 R543 protein - rat
929 142 2 T25879 hypothetical prote
930 143 2 A26918 procyclic acidic r
931 143 2 S59506 ferric pseudobacti
932 143 2 AC1730 hypothetical prote
933 143 2 A81251 probable transcrip
934 144 2 D98172 gamma carboxymuon
935 144 2 AI3114 gamma carboxymuon
936 144 2 AC1907 hypothetical prote
937 144 2 A44418 procyclin PSSA-1 -
938 145 2 A83010 conserved hypothet
939 145 2 C70328 conserved hypothet
940 145 2 H75108 hypothetical prote
941 145 2 H86517 hypothetical prote
942 145 2 G72103 hypothetical prote
943 145 2 T49888 hypothetical prote
944 145 2 T06156 hypothetical prote
945 145 2 AI1071 DNA polymerase III
946 145 2 T08000 translation initia
947 146 1 GGNK1B globin I - ark she
948 146 1 GGNK1D secretory protein
949 146 2 S70202 secretory protein
950 146 2 E72673 VtP8H12-12 (impor
951 146 2 C86187 VtP8H12-12 (impor
952 147 2 S36144 hemoglobin I - ark
953 147 2 I46467 luteinizing hormon
954 147 2 D69368 conserved hypothet
955 147 2 S67304 probable membrane
956 147 2 T32403 hypothetical prote
957 147 2 C70312 hypothetical prote
958 147 2 B87607 hypothetical prote
959 148 2 S22088 hypothetical prote
960 148 2 D82623 conserved hypothet
961 148 2 F97524 DNAA suppressor pr
962 148 2 S41026 hypothetical prote
963 148 2 C84650 probable membrane
964 148 2 E75300 conserved hypothet
965 148 2 AF1119 PTS system, enzyme
966 148 2 AI1179 PTS system, enzyme
967 149 1 R5EC9 ribosomal protein
968 149 2 AB1053 50S ribosomal chai
969 149 2 C86117 50S ribosomal subu
970 149 2 C91276 50S ribosomal subu
971 149 2 C82333 ribosomal protein
972 149 2 D64076 ribosomal protein
973 149 2 D83256 heat-shock protein
974 149 2 E90230 partial transposas
975 149 2 T33604 hypothetical prote
976 149 2 AF2713 conserved hypothet
977 150 1 E64249 pinin repressor pi
978 150 2 AI0429 50S ribosomal prot

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979      5      3.8      150      2      C96647      hypothetical prote
980      5      3.8      150      2      G85939      type III secretion
981      5      3.8      150      2      AC0303      hypothetical prote
982      5      3.8      151      1      Q2BPP4      hypothetical prote
983      5      3.8      151      1      S73506      piliB homolog K05_o
984      5      3.8      151      2      D64319      probable format'e d
985      5      3.8      151      2      AC0495      probable acetyltra
986      5      3.8      151      2      T10196      hypothetical prote
987      5      3.8      151      2      S69472      hypothetical prote
988      5      3.8      151      2      B70862      hypothetical prote
989      5      3.8      151      2      E95378      SvrB regulatory pr
990      5      3.8      151      2      S52598      probable membrane
991      5      3.8      151      2      T19087      hypothetical prote
992      5      3.8      151      2      AB3263      thiol/disulfide in
993      5      3.8      152      2      AD0256      probable prophage
994      5      3.8      152      2      H87244      50S ribosomal prot
995      5      3.8      152      2      F90543      conserved hypothet
996      5      3.8      152      2      F86473      hypothetical prote
997      5      3.8      152      2      T19905      hypothetical prote
998      5      3.8      153      2      JX0072      troponin C, striat
999      5      3.8      153      2      JH0247      guanine nucleotide
1000     5      3.8      153      2      B84036      hypothetical prote

ALIGNMENTS

RESULT 1
S42384
Kruppel-like protein - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 09-Sep-1997
C:Accession: S42384
R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42384
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <SMI>
A:Cross-references: EMBL:Z30662; NID:9459581; PID:9459587
C:Genetics:
A:Introns: 10/3; 48/3; 182/3; 315/3; 360/3

Query Match      30.3%; Score 40; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 3.1e-34;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      80      EETKAMESQRAYRFVQKDWGFKFIRRDFLLDDEANGLLP 119
      |||||
Db      134      EETKAMESQRAYRFVQKDWGFKFIRRDFLLDDEANGLLP 173

RESULT 2
B64956
flagellar protein flis - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: B64956
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: B64956
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-136 <BLAT>
A:Cross-references: UNIPROT:P26608; GB:AE000285; GB:U00096; NID:gl7882229; PIDN:AAC74992.
C:Genetics:
A:Gene: flis
C:Superfamily: flagellar protein flis

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C:Keywords: flagellum

Query Match      5.3%; Score 7; DB 1; Length 136;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      44      LDEESKD 50
      |||||
Db      73      LDEESKD 79

RESULT 3
H90961
flagellar protein Flis [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050
C:Species: Escherichia coli
C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C:Accession: H90961
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: H90961
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <HAY>
A:Cross-references: UNIPROT:Q8XBB7; GB:BA000007; PIDN:BA836087.1; PID:gl13362132; GSPDB:G
A:Experimental source: strain O157:H7, substrain RIMD 0509952
C:Genetics:
A:Gene: ECs2664
C:Superfamily: flagellar protein flis

Query Match      5.3%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      44      LDEESKD 50
      |||||
Db      73      LDEESKD 79

RESULT 4
H85809
hypothetical protein flis [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:Accession: H85809
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: H85809
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <STO>
A:Cross-references: UNIPROT:Q8XBB7; GB:AE005174; NID:gl2516026; PIDN:AAG56940.1; GSPDB:G
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: flis
C:Superfamily: flagellar protein flis

Query Match      5.3%; Score 7; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      44      LDEESKD 50
      |||||
Db      73      LDEESKD 79

RESULT 5
A71051

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hypothetical protein PH1104 - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C:Accession: A71051
 R:Kawarayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
 M.; Ohkuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: A71051
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-143 <KAW>
 A:Cross-references: UNIPROT:O58831; GB:AP000005; NID:G3236132; PIDN:BA30203.1; PID:G325
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1104

Query Match 5.3%; Score 7; DB 2; Length 143;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 54 LYLKLV 60
 |||||
 Db 44 LYLKLV 50

RESULT 6
 F82133
 hypothetical protein VC1991 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
 C:Accession: F82133
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, R.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: F82133
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-145 <HEI>
 A:Cross-references: UNIPROT:Q9KQK7; GB:AE004273; GB:AE003852; NID:G9656517; PIDN:AAF9513
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1991
 A:Map position: 1

Query Match 5.3%; Score 7; DB 2; Length 145;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 FSSGAND 31
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 Db 31 FSSGAND 37

RESULT 7
 JC6050
 homoserine kinase (EC 2.7.1.39) - Lactococcus lactis
 C:Species: Lactococcus lactis
 C>Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 09-Jul-2004
 C:Accession: JC6050
 R:Madgen, S.M.; Albrechtsen, B.; Hansen, E.B.; Israelsen, H.
 J. Bacteriol. 178, 3689-3694, 1996
 A:Title: Cloning and transcriptional analysis of two threonine biosynthetic genes from L
 A:Reference number: JC6049; MUID:96272237; PMID:8682767
 A:Accession: JC6050
 A:Molecule type: mRNA
 A:Residues: 1-296 <MAD>
 A:Cross-references: UNIPROT:P52991; EMBL:X96988; NID:G1255938; PIDN:CAA65714.1; PID:G125

C:Genetics:
 A:Gene: thrB
 C:Function:
 A:Description: catalyzes the conversion of homoserine to threonine
 A:Pathway: threonine biosynthesis
 C:Superfamily: homoserine kinase
 C:Keywords: phosphotransferase; threonine biosynthesis

Query Match 5.3%; Score 7; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 119 PDDKLT 125
 |||||
 Db 259 PDDKLT 265

RESULT 8
 H86769
 homoserine kinase (EC 2.7.1.39) [imported] - Lactococcus lactis subsp. lactis (strain IL
 C:Species: Lactococcus lactis subsp. lactis
 C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
 C:Accession: H86769
 R:Boletini, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
 Genome Res. 11, 731-753, 2001
 A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ss
 A:Reference number: A86625; MUID:21235186; PMID:11337471
 A:Accession: H86769
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-296 <STO>
 A:Cross-references: UNIPROT:Q9GCD7; GB:AE005176; PID:G12724124; PIDN:AAK05258.1; GSPDB:C
 A:Experimental source: strain IL1403
 C:Genetics:
 A:Gene: thrB
 C:Superfamily: homoserine kinase
 C:Keywords: phosphotransferase

Query Match 5.3%; Score 7; DB 2; Length 296;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LLPDDKL 123
 |||||
 Db 257 LLPDDKL 263

RESULT 9
 H95075
 hypothetical protein SP0656 [imported] - Streptococcus pneumoniae (strain TIGR4)
 C:Species: Streptococcus pneumoniae
 C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 09-Jul-2004
 C:Accession: H95075
 R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple,
 son, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
 A:Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: H95075
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-302 <KUR>
 A:Cross-references: UNIPROT:Q97RX7; GB:AE005672; PIDN:AAK74801.1; PID:G14972128; GSPDB:C
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SP0656

Query Match 5.3%; Score 7; DB 2; Length 302;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      46  EESKDYL 52
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Db      28  EESKDYL 34

RESULT 10
D69744
conserved hypothetical protein ybbI - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C/Accession: D69744
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berte
R.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Enian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
A/Authors: Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
leoch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivoita, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terptrata, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; MUID:98044033; PMID:9384377
A/Accession: D69744
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-304 <KUN>
A/Cross-references: UNIPROT:Q45582; GB:Z99104; GB:AL009126; NID:g26322267; PIDN:CAB11946.
A/Experimental source: strain 168
C/Genetics:
A/Gene: ybbI
C/Superfamily: conserved hypothetical protein b2428

      Query Match      5.3%; Score 7; DB 2; Length 304;
      Best Local Similarity 100.0%; Pred. No. 24;
      Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      110  LLEANG 116
      |||||
Db      287  LLEANG 293

RESULT 11
C83088
hypothetical protein PA4467 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C/Accession: C83088
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: C83088
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-310 <STO>
A/Cross-references: UNIPROT:Q9HVW1; GB:AE004860; GB:AE004091; NID:g9950692; PIDN:AAG0785
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA4467

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Qy      111  LDEANGL 117
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Db      195  LDEANGL 201

RESULT 12
A99196
purine nucleosidase, probable (iunH-1) [imported] - Sulfolobus solfataricus
C/Species: Sulfolobus solfataricus
C/Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: A99196
R/She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan,
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A/Description: Sulfolobus solfataricus complete genome.
A/Reference number: A99139
A/Accession: A99196
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-311 <KUR>
A/Cross-references: UNIPROT:Q97ZS5; GB:AE006641; NID:gl3813662; PIDN:AAK40824.1; GSPDB:GI
C/Genetics:
A/Gene: iunH-1
C/Superfamily: yaaF protein

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Qy      52  LSLYLL 58
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Db      16  LSLYLL 22

RESULT 13
T45994
hypothetical protein F9D24.250 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
C/Accession: T45994
R/D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
submitted to the Protein Sequence Database, January 2000
A/Reference number: Z23011
A/Accession: T45994
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-325 <DAN>
A/Cross-references: UNIPROT:Q9M212; EMBL:AL137081
A/Experimental source: cultivar Columbia; BAC clone F9D24
C/Genetics:
A/Map position: 3
A/Introns: 36/2; 89/1; 198/3
A/Note: F9D24.250
C/Superfamily: Arabidopsis thaliana hypothetical protein F9D24.110

      Query Match      5.3%; Score 7; DB 2; Length 325;
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Db      48  DYLSLYL 54

RESULT 14
G75540
Elac family protein - Deinococcus radiodurans (strain R1)
C/Species: Deinococcus radiodurans
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C/Accession: G75540
R/White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999

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A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A;Reference number: A75250; MUID:20036896; PMID:10567266
 A;Accession: G75540
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-331 <WHI>
 A;Cross-references: UNIPROT:Q9RXP0; GB:AE001888; GB:AE000513; NID:g6457936; PIDN:AAF0985
 A;Experimental source: strain R1
 C;Genetics:
 A;Gene: DR0270
 A;Map position: 1
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RESULT 15

G69474
 conserved hypothetical protein AF1800 - Archaeoglobus fulgidus
 C;Species: Archaeoglobus fulgidus
 C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
 C;Accession: G69474
 R;Klenk, H.P.; Clayton, R.A.; Tomb, J.P.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
 ; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
 Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
 Nature 390, 364-370, 1997
 A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
 Smith, H.O.; Woese, C.R.; Venter, J.C.
 A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
 A;Reference number: A69250; MUID:98049343; PMID:9389475
 A;Accession: G69474
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-340 <KLE>
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 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 53 SLXLLLV 59
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 Db 246 SLXLLLV 252

Search completed: July 20, 2005, 20:52:48
 Job time : 34.8571 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:38:46 ; Search time 24.8286 Seconds
(without alignments)
396.868 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

Sequence: 1 SYMTINNFSRCREEMGEVI.....EANGLLPDKLTLCFVSVV 132

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents_AA.*

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	7	5.3	166	4	US-09-519-232-54
7	7	5.3	227	4	US-09-270-767-58283
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13	7	5.3	567	4	US-09-538-092-1365
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23	6	4.5	35	2	US-08-436-420-2
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Sequence 27894, A
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Sequence 208, App
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Sequence 18862, A
Sequence 6201, Ap
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Sequence 35784, A
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Sequence 45726, A
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Sequence 3883, Ap
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Sequence 22, Appli

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140	6	4.5	327	1	US-08-932-787B-19	Sequence 35, Appl	213	6	4.5	794	4	US-09-949-016-9883	Sequence 9883, Ap
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142	6	4.5	327	4	US-09-248-796A-19580	Sequence 1958, A	215	6	4.5	810	4	US-09-489-039A-9748	Sequence 9748, Ap
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145	6	4.5	353	2	US-08-461-985-14	Sequence 14, Appl	218	6	4.5	875	4	US-09-585-858-18	Sequence 18, Appl
146	6	4.5	353	3	US-08-932-787B-19	Sequence 19, Appl	219	6	4.5	875	4	US-10-270-878-18	Sequence 18, Appl
147	6	4.5	353	3	US-08-932-787B-19	Sequence 19, Appl	220	6	4.5	892	1	US-07-977-434-12	Sequence 12, Appl
148	6	4.5	353	3	US-08-888-818C-19	Sequence 19, Appl	221	6	4.5	892	1	US-08-458-819-12	Sequence 12, Appl
149	6	4.5	355	4	US-09-583-110-3542	Sequence 3542, Ap	222	6	4.5	892	5	PCT-US91-07035-12	Sequence 12, Appl
150	6	4.5	356	4	US-09-107-532A-6286	Sequence 6286, Ap	223	6	4.5	898	4	US-09-252-991A-23689	Sequence 23689, A
151	6	4.5	361	4	US-09-107-433-3933	Sequence 3933, Ap	224	6	4.5	945	4	US-09-198-452A-1030	Sequence 1030, Ap
152	6	4.5	364	4	US-09-205-258-1008	Sequence 1008, Ap	225	6	4.5	946	4	US-09-252-991A-18989	Sequence 18989, A
153	6	4.5	373	4	US-09-252-991A-24545	Sequence 24545, A	226	6	4.5	950	4	US-09-438-185A-959	Sequence 959, App
154	6	4.5	376	4	US-09-543-681A-6740	Sequence 6740, Ap	227	6	4.5	973	2	US-08-683-262B-75	Sequence 75, Appl
155	6	4.5	376	4	US-09-949-016-9185	Sequence 9185, Ap	228	6	4.5	973	3	US-09-361-707-75	Sequence 75, Appl
156	6	4.5	382	4	US-09-134-000C-3829	Sequence 3829, Ap	229	6	4.5	989	4	US-09-540-236-2137	Sequence 2137, Ap
157	6	4.5	383	4	US-09-543-681A-7432	Sequence 7432, Ap	230	6	4.5	998	4	US-09-949-016-8326	Sequence 8326, Ap
158	6	4.5	397	1	US-07-956-697B-5	Sequence 5, Appli	231	6	4.5	1003	1	US-08-571-758-4	Sequence 4, Appli
159	6	4.5	397	1	US-08-263-098-5	Sequence 5, Appli	232	6	4.5	1003	1	US-08-909-984A-4	Sequence 4, Appli
160	6	4.5	401	4	US-09-489-039A-7926	Sequence 7926, Ap	233	6	4.5	1003	1	US-08-909-983-4	Sequence 4, Appli
161	6	4.5	401	4	US-09-252-991A-27198	Sequence 27198, A	234	6	4.5	1036	4	US-10-014-882-2	Sequence 2, Appli
162	6	4.5	422	2	US-08-712-072C-2	Sequence 2, Appli	235	6	4.5	1036	4	US-10-419-279-2	Sequence 2, Appli
163	6	4.5	430	4	US-09-134-000C-5725	Sequence 5725, Ap	236	6	4.5	1093	4	US-09-949-016-11535	Sequence 11535, A
164	6	4.5	436	4	US-09-198-452A-451	Sequence 451, App	237	6	4.5	1093	5	PCT-US93-03077-1	Sequence 1, Appli
165	6	4.5	442	4	US-09-489-039A-11693	Sequence 11693, A	238	6	4.5	1141	1	US-08-363-300-2	Sequence 2, Appli
166	6	4.5	454	3	US-09-518-046-2	Sequence 2, Appli	239	6	4.5	1151	1	US-08-286-889-37	Sequence 37, Appl
167	6	4.5	455	3	US-09-261-416-2	Sequence 2, Appli	240	6	4.5	1151	1	US-08-485-618-37	Sequence 37, Appl
168	6	4.5	455	4	US-08-583-110-3905	Sequence 3905, Ap	241	6	4.5	1151	1	US-08-362-652-37	Sequence 37, Appl
169	6	4.5	458	4	US-08-487-596-16	Sequence 16, Appl	242	6	4.5	1151	2	US-08-605-672-37	Sequence 37, Appl
170	6	4.5	458	4	US-08-484-722-4	Sequence 4, Appli	243	6	4.5	1151	2	US-08-482-293A-37	Sequence 37, Appl
171	6	4.5	458	4	US-08-660-451A-16	Sequence 16, Appl	244	6	4.5	1151	2	US-08-943-363-37	Sequence 37, Appl
172	6	4.5	458	4	US-09-949-016-5986	Sequence 5986, Ap	245	6	4.5	1151	3	US-09-193-043-37	Sequence 37, Appl
173	6	4.5	461	4	US-09-248-796A-16346	Sequence 16346, A	246	6	4.5	1151	4	US-09-688-307A-37	Sequence 37, Appl

247	6	4.5	1151	4	US-09-252-991A-23596	Sequence 23596, A	320	5	3.8	12	4	US-09-403-752A-62	Sequence 62, Appl
248	6	4.5	1151	4	US-09-350-259-37	Sequence 37, Appl	321	5	3.8	12	4	US-09-551-151A-62	Sequence 62, Appl
249	6	4.5	1155	1	US-08-286-889-46	Sequence 46, Appl	322	5	3.8	14	4	US-09-342-325C-64	Sequence 64, Appl
250	6	4.5	1155	1	US-08-485-618-46	Sequence 46, Appl	323	5	3.8	15	2	US-08-428-257A-68	Sequence 68, Appl
251	6	4.5	1155	1	US-08-362-652-46	Sequence 46, Appl	324	5	3.8	15	3	US-08-602-999A-406	Sequence 406, App
252	6	4.5	1155	2	US-08-605-672-46	Sequence 46, Appl	325	5	3.8	16	4	US-09-556-877-39	Sequence 39, Appl
253	6	4.5	1155	2	US-08-482-293A-46	Sequence 46, Appl	326	5	3.8	16	4	US-09-500-124-406	Sequence 406, App
254	6	4.5	1155	2	US-08-943-363-46	Sequence 46, Appl	327	5	3.8	16	4	US-09-288-594A-39	Sequence 39, Appl
255	6	4.5	1155	3	US-09-193-043-46	Sequence 46, Appl	328	5	3.8	16	4	US-09-620-412C-39	Sequence 39, Appl
256	6	4.5	1155	4	US-09-688-307A-46	Sequence 46, Appl	329	5	3.8	16	4	US-09-410-568-39	Sequence 39, Appl
257	6	4.5	1155	4	US-09-350-259-46	Sequence 46, Appl	330	5	3.8	16	4	US-09-598-419-39	Sequence 39, Appl
258	6	4.5	1155	4	US-09-328-352-6826	Sequence 6826, Ap	331	5	3.8	16	4	US-09-920-174-30	Sequence 30, Appl
259	6	4.5	1161	1	US-08-485-618-53	Sequence 53, Appl	332	5	3.8	16	4	US-09-920-195A-30	Sequence 30, Appl
260	6	4.5	1161	1	US-08-485-618-55	Sequence 55, Appl	333	5	3.8	19	2	US-08-318-837-35	Sequence 25, Appl
261	6	4.5	1161	1	US-08-362-652-53	Sequence 53, Appl	334	5	3.8	19	4	US-09-556-877-93	Sequence 93, Appl
262	6	4.5	1161	1	US-08-362-652-55	Sequence 55, Appl	335	5	3.8	19	4	US-09-620-412C-93	Sequence 93, Appl
263	6	4.5	1161	2	US-08-605-672-53	Sequence 53, Appl	336	5	3.8	19	4	US-09-410-568-93	Sequence 93, Appl
264	6	4.5	1161	2	US-08-605-672-55	Sequence 55, Appl	337	5	3.8	19	4	US-09-598-419-93	Sequence 93, Appl
265	6	4.5	1161	2	US-08-482-293A-53	Sequence 53, Appl	338	5	3.8	20	1	US-07-787-148C-1	Sequence 1, Appl
266	6	4.5	1161	2	US-08-482-293A-55	Sequence 55, Appl	339	5	3.8	20	1	US-08-103-742-23	Sequence 23, Appl
267	6	4.5	1161	2	US-08-943-363-53	Sequence 53, Appl	340	5	3.8	20	1	US-08-199-508-19	Sequence 19, Appl
268	6	4.5	1161	2	US-08-943-363-55	Sequence 55, Appl	341	5	3.8	20	1	US-08-199-508-20	Sequence 20, Appl
269	6	4.5	1161	3	US-09-193-043-53	Sequence 53, Appl	342	5	3.8	20	2	US-08-584-972-61	Sequence 61, Appl
270	6	4.5	1161	3	US-09-193-043-55	Sequence 55, Appl	343	5	3.8	20	2	US-08-499-676A-39	Sequence 39, Appl
271	6	4.5	1161	3	US-09-688-307A-53	Sequence 53, Appl	344	5	3.8	20	3	US-09-208-277-13	Sequence 13, Appl
272	6	4.5	1161	4	US-09-350-259-53	Sequence 53, Appl	345	5	3.8	20	4	US-09-556-877-13	Sequence 13, Appl
273	6	4.5	1161	4	US-09-350-259-55	Sequence 55, Appl	346	5	3.8	20	4	US-09-556-877-94	Sequence 94, Appl
274	6	4.5	1161	4	US-09-350-259-55	Sequence 55, Appl	347	5	3.8	20	4	US-09-556-877-95	Sequence 95, Appl
275	6	4.5	1192	4	US-09-902-540-14526	Sequence 14526, A	348	5	3.8	20	4	US-09-556-877-98	Sequence 98, Appl
276	6	4.5	1220	2	US-08-680-346-38	Sequence 38, Appl	349	5	3.8	20	4	US-09-288-594A-13	Sequence 13, Appl
277	6	4.5	1276	3	US-09-297-937C-13	Sequence 13, Appl	350	5	3.8	20	4	US-09-620-412C-13	Sequence 13, Appl
278	6	4.5	1337	3	US-08-854-585-2	Sequence 2, Appl	351	5	3.8	20	4	US-09-620-412C-94	Sequence 94, Appl
279	6	4.5	1337	4	US-09-447-533-2	Sequence 2, Appl	352	5	3.8	20	4	US-09-620-412C-95	Sequence 95, Appl
280	6	4.5	1337	5	PCT-US95-05512-2	Sequence 2, Appl	353	5	3.8	20	4	US-09-620-412C-98	Sequence 98, Appl
281	6	4.5	1427	4	US-09-538-032-1044	Sequence 1044, Ap	354	5	3.8	20	4	US-09-410-568-13	Sequence 13, Appl
282	6	4.5	1466	4	US-09-262-537-20	Sequence 20, Appl	355	5	3.8	20	4	US-09-410-568-94	Sequence 94, Appl
283	6	4.5	1469	4	US-09-262-537-58	Sequence 58, Appl	356	5	3.8	20	4	US-09-410-568-95	Sequence 95, Appl
284	6	4.5	1471	4	US-08-811-519-1	Sequence 1, Appl	357	5	3.8	20	4	US-09-410-568-98	Sequence 98, Appl
285	6	4.5	1673	4	US-09-418-710-70	Sequence 70, Appl	358	5	3.8	20	4	US-09-598-419-13	Sequence 13, Appl
286	6	4.5	1673	4	US-09-839-479-69	Sequence 69, Appl	359	5	3.8	20	4	US-09-598-419-94	Sequence 94, Appl
287	6	4.5	1674	4	US-09-418-710-1	Sequence 1, Appl	360	5	3.8	20	4	US-09-598-419-95	Sequence 95, Appl
288	6	4.5	1674	4	US-09-839-479-1	Sequence 1, Appl	361	5	3.8	20	4	US-09-598-419-98	Sequence 98, Appl
289	6	4.5	1706	2	US-08-459-568-2	Sequence 2, Appl	362	5	3.8	20	4	US-09-889-136-5	Sequence 5, Appl
290	6	4.5	1706	2	US-08-399-411-2	Sequence 2, Appl	363	5	3.8	21	2	US-08-194-881E-41	Sequence 41, Appl
291	6	4.5	1706	3	US-08-516-859A-2	Sequence 2, Appl	364	5	3.8	21	3	US-08-499-676A-20	Sequence 20, Appl
292	6	4.5	1706	3	US-09-586-472-2	Sequence 2, Appl	365	5	3.8	21	3	US-08-860-089-2	Sequence 2, Appl
293	6	4.5	1706	4	US-09-528-706-2	Sequence 2, Appl	366	5	3.8	22	1	US-07-755-461A-8	Sequence 8, Appl
294	6	4.5	1724	1	US-08-325-547-3	Sequence 3, Appl	367	5	3.8	22	1	US-08-662-318-8	Sequence 8, Appl
295	6	4.5	1780	4	US-09-949-016-6899	Sequence 6899, Ap	368	5	3.8	22	2	US-08-662-318-8	Sequence 8, Appl
296	6	4.5	1783	4	US-09-362-336A-2	Sequence 2, Appl	369	5	3.8	22	2	US-08-499-676A-40	Sequence 40, Appl
297	6	4.5	1786	4	US-09-949-016-7880	Sequence 7880, Ap	370	5	3.8	22	4	US-09-549-831-3	Sequence 3, Appl
298	6	4.5	1804	4	US-09-362-336A-4	Sequence 4, Appl	371	5	3.8	22	4	US-08-838-128B-31	Sequence 31, Appl
299	6	4.5	3241	4	US-09-841-786-1	Sequence 1, Appl	372	5	3.8	22	4	US-08-838-128B-31	Sequence 31, Appl
300	5	3.8	5	4	US-09-800-170-53	Sequence 53, Appl	373	5	3.8	22	5	PCT-US95-12509-8	Sequence 8, Appl
301	5	3.8	7	1	US-08-233-788A-49	Sequence 49, Appl	374	5	3.8	23	2	US-08-310-912A-103	Sequence 103, App
302	5	3.8	8	4	US-09-920-174-29	Sequence 29, Appl	375	5	3.8	23	3	US-08-841-089-103	Sequence 103, App
303	5	3.8	8	4	US-09-920-195A-29	Sequence 29, Appl	376	5	3.8	23	3	US-09-301-085-103	Sequence 103, App
304	5	3.8	9	1	US-08-615-181-37	Sequence 37, Appl	377	5	3.8	23	5	PCT-US95-04570-103	Sequence 103, App
305	5	3.8	9	3	US-08-159-339A-631	Sequence 631, App	378	5	3.8	23	5	PCT-US95-04570-103	Sequence 103, App
306	5	3.8	9	3	US-09-518-046-102	Sequence 102, App	379	5	3.8	24	3	US-07-942-345-295	Sequence 295, App
307	5	3.8	10	2	US-08-428-257A-44	Sequence 44, Appl	380	5	3.8	26	1	US-07-942-345-296	Sequence 296, App
308	5	3.8	10	3	US-08-405-647B-34	Sequence 34, Appl	381	5	3.8	26	1	US-07-942-345-333	Sequence 333, App
309	5	3.8	10	3	US-08-985-499-34	Sequence 34, Appl	382	5	3.8	26	1	US-07-942-345-333	Sequence 333, App
310	5	3.8	10	4	US-09-305-542A-17	Sequence 17, Appl	383	5	3.8	26	4	US-09-122-144-10	Sequence 10, Appl
311	5	3.8	10	5	PCT-US96-03180-34	Sequence 34, Appl	384	5	3.8	26	4	US-08-838-128B-29	Sequence 29, Appl
312	5	3.8	11	2	US-08-811-897A-3	Sequence 3, Appl	385	5	3.8	27	1	US-08-451-307-25	Sequence 25, Appl
313	5	3.8	11	2	US-08-855-213-3	Sequence 3, Appl	386	5	3.8	27	1	US-08-066-325-82	Sequence 82, Appl
314	5	3.8	11	3	US-09-201-474-3	Sequence 3, Appl	387	5	3.8	27	1	US-08-336-618-1	Sequence 1, Appl
315	5	3.8	11	4	US-09-721-908-16	Sequence 16, Appl	388	5	3.8	28	3	US-09-082-279B-673	Sequence 673, App
316	5	3.8	12	1	US-07-798-776-9	Sequence 9, Appl	389	5	3.8	28	3	US-09-315-304B-673	Sequence 673, App
317	5	3.8	12	3	US-08-251-288A-9	Sequence 9, Appl	390	5	3.8	28	4	US-09-228-900-77	Sequence 77, Appl
318	5	3.8	12	3	US-09-298-819A-9	Sequence 9, Appl	391	5	3.8	28	4	US-09-834-784-673	Sequence 673, App
319	5	3.8	12	3	US-08-860-089-3	Sequence 3, Appl	392	5	3.8	28	4	US-09-442-989-23	Sequence 23, Appl

393	5	3.8	28	4	US-09-515-965A-673	Sequence 673, App	466	5	3.8	35	3	US-09-082-279B-650	Sequence 650, App
394	5	3.8	28	4	US-09-528-200-134	Sequence 134, App	467	5	3.8	35	3	US-09-082-279B-651	Sequence 651, App
395	5	3.8	28	4	US-09-350-641C-673	Sequence 673, App	468	5	3.8	35	3	US-09-082-279B-677	Sequence 677, App
396	5	3.8	28	4	US-09-350-841A-673	Sequence 673, App	469	5	3.8	35	3	US-09-324-455-10	Sequence 10, App1
397	5	3.8	29	1	US-08-218-023-7	Sequence 7, App1	470	5	3.8	35	3	US-08-474-349A-447	Sequence 447, App
398	5	3.8	29	2	US-08-194-981E-39	Sequence 39, App1	471	5	3.8	35	3	US-08-474-349A-448	Sequence 448, App
399	5	3.8	29	2	US-08-194-981E-42	Sequence 42, App1	472	5	3.8	35	3	US-08-474-349A-449	Sequence 449, App
400	5	3.8	29	2	US-08-194-981E-44	Sequence 44, App1	473	5	3.8	35	3	US-08-474-349A-450	Sequence 450, App
401	5	3.8	29	4	US-09-149-476-513	Sequence 513, App	474	5	3.8	35	3	US-08-474-349A-451	Sequence 451, App
402	5	3.8	30	1	US-08-447-411-33	Sequence 33, App1	475	5	3.8	35	3	US-08-474-349A-452	Sequence 452, App
403	5	3.8	30	2	US-08-480-473B-35	Sequence 35, App1	476	5	3.8	35	3	US-08-474-349A-453	Sequence 453, App
404	5	3.8	30	3	US-08-915-213-35	Sequence 35, App1	477	5	3.8	35	3	US-08-474-349A-454	Sequence 454, App
405	5	3.8	30	3	US-09-235-217-35	Sequence 35, App1	478	5	3.8	35	3	US-08-474-349A-455	Sequence 455, App
406	5	3.8	30	4	US-09-402-532-9	Sequence 9, App1	479	5	3.8	35	3	US-08-474-349A-456	Sequence 456, App
407	5	3.8	30	5	PTT-US96-10251-35	Sequence 35, App1	480	5	3.8	35	3	US-08-474-349A-457	Sequence 457, App
408	5	3.8	31	1	US-08-190-802A-254	Sequence 254, App	481	5	3.8	35	3	US-08-474-349A-458	Sequence 458, App
409	5	3.8	31	3	US-08-477-346-254	Sequence 254, App	482	5	3.8	35	3	US-08-474-349A-459	Sequence 459, App
410	5	3.8	31	3	US-08-473-089-254	Sequence 254, App	483	5	3.8	35	3	US-08-474-349A-460	Sequence 460, App
411	5	3.8	31	3	US-09-513-342-22	Sequence 22, App1	484	5	3.8	35	3	US-08-474-349A-461	Sequence 461, App
412	5	3.8	31	4	US-08-487-072A-254	Sequence 254, App	485	5	3.8	35	3	US-08-474-349A-462	Sequence 462, App
413	5	3.8	31	4	US-08-437-943D-102	Sequence 102, App	486	5	3.8	35	3	US-08-474-349A-463	Sequence 463, App
414	5	3.8	31	4	US-08-437-943D-103	Sequence 103, App	487	5	3.8	35	3	US-08-474-349A-464	Sequence 464, App
415	5	3.8	31	4	US-08-437-943D-104	Sequence 104, App	488	5	3.8	35	3	US-09-315-304B-418	Sequence 418, App
416	5	3.8	31	4	US-08-437-943D-105	Sequence 105, App	489	5	3.8	35	3	US-09-315-304B-419	Sequence 419, App
417	5	3.8	31	4	US-08-437-943D-106	Sequence 106, App	490	5	3.8	35	3	US-09-315-304B-420	Sequence 420, App
418	5	3.8	31	4	US-08-437-943D-107	Sequence 107, App	491	5	3.8	35	3	US-09-315-304B-421	Sequence 421, App
419	5	3.8	31	4	US-08-437-943D-108	Sequence 108, App	492	5	3.8	35	3	US-09-315-304B-422	Sequence 422, App
420	5	3.8	31	4	US-08-437-943D-109	Sequence 109, App	493	5	3.8	35	3	US-09-315-304B-423	Sequence 423, App
421	5	3.8	31	4	US-08-437-943D-110	Sequence 110, App	494	5	3.8	35	3	US-09-315-304B-424	Sequence 424, App
422	5	3.8	31	4	US-08-437-943D-111	Sequence 111, App	495	5	3.8	35	3	US-09-315-304B-425	Sequence 425, App
423	5	3.8	32	4	US-09-270-767-32021	Sequence 32021, A	496	5	3.8	35	3	US-09-315-304B-426	Sequence 426, App
424	5	3.8	32	4	US-09-270-767-47238	Sequence 47238, A	497	5	3.8	35	3	US-09-315-304B-427	Sequence 427, App
425	5	3.8	32	2	US-08-499-676A-34	Sequence 34, App1	498	5	3.8	35	3	US-09-315-304B-428	Sequence 428, App
426	5	3.8	33	4	US-09-402-532-10	Sequence 10, App1	499	5	3.8	35	3	US-09-315-304B-429	Sequence 429, App
427	5	3.8	34	3	US-09-082-279B-737	Sequence 737, App	500	5	3.8	35	3	US-09-315-304B-430	Sequence 430, App
428	5	3.8	34	3	US-09-315-304B-737	Sequence 737, App	501	5	3.8	35	3	US-09-315-304B-431	Sequence 431, App
429	5	3.8	34	4	US-09-228-990-71	Sequence 71, App1	502	5	3.8	35	3	US-09-315-304B-432	Sequence 432, App
430	5	3.8	34	4	US-08-834-784-737	Sequence 737, App	503	5	3.8	35	3	US-09-315-304B-433	Sequence 433, App
431	5	3.8	34	4	US-09-442-989-20	Sequence 20, App1	504	5	3.8	35	3	US-09-315-304B-434	Sequence 434, App
432	5	3.8	34	4	US-09-515-965A-737	Sequence 737, App	505	5	3.8	35	3	US-09-315-304B-435	Sequence 435, App
433	5	3.8	34	4	US-09-350-641C-737	Sequence 737, App	506	5	3.8	35	3	US-09-315-304B-646	Sequence 646, App
434	5	3.8	34	4	US-09-350-841A-737	Sequence 737, App	507	5	3.8	35	3	US-09-315-304B-647	Sequence 647, App
435	5	3.8	35	3	US-08-471-913A-210	Sequence 210, App	508	5	3.8	35	3	US-09-315-304B-648	Sequence 648, App
436	5	3.8	35	3	US-08-471-913A-211	Sequence 211, App	509	5	3.8	35	3	US-09-315-304B-649	Sequence 649, App
437	5	3.8	35	3	US-09-014-416-28	Sequence 28, App1	510	5	3.8	35	3	US-09-315-304B-650	Sequence 650, App
438	5	3.8	35	3	US-09-014-416-30	Sequence 30, App1	511	5	3.8	35	3	US-09-315-304B-651	Sequence 651, App
439	5	3.8	35	3	US-09-014-416-32	Sequence 32, App1	512	5	3.8	35	3	US-09-315-304B-677	Sequence 677, App
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441	5	3.8	35	3	US-09-014-416-37	Sequence 37, App1	514	5	3.8	35	4	US-08-485-546A-211	Sequence 211, App
442	5	3.8	35	3	US-09-014-416-38	Sequence 38, App1	515	5	3.8	35	4	US-09-834-784-418	Sequence 418, App
443	5	3.8	35	3	US-09-014-416-41	Sequence 41, App1	516	5	3.8	35	4	US-09-834-784-419	Sequence 419, App
444	5	3.8	35	3	US-09-082-279B-418	Sequence 418, App	517	5	3.8	35	4	US-09-834-784-420	Sequence 420, App
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547	5	3.8	35	4	US-09-515-965A-425	Sequence 425, App	620	5	3.8	36	5	PCT-US93-08528-242	Sequence 242, App
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574	5	3.8	35	4	US-09-350-641C-426	Sequence 426, App	647	5	3.8	45	3	US-08-471-913A-203	Sequence 203, App
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577	5	3.8	35	4	US-09-350-641C-429	Sequence 429, App	650	5	3.8	45	3	US-08-474-349A-203	Sequence 203, App
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608	5	3.8	35	4	US-09-350-841A-434	Sequence 434, App	681	5	3.8	49	3	US-09-482-273-180	Sequence 180, App
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ALIGNMENTS

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RESULT 1
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; Sequence 9724, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9724
; LENGTH: 385
; TYPE: PRT
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US-09-949-016-9724
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; Sequence 42959, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
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; SEQ ID NO 42959
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US-09-270-767-42959
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RESULT 3

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; Sequence 7, Application US/08861476C
; Patent No. 6447786
; GENERAL INFORMATION:
; APPLICANT: New York University Medical Center
; TITLE OF INVENTION: BLOCKING EXPRESSION OF VIRULENCE FACTORS IN S. AUREUS
; FILE REFERENCE: 63753/7
; CURRENT APPLICATION NUMBER: US/08/861,476C
; CURRENT FILING DATE: 1997-05-22
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US-08-861-476C-7
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; Patent No. 6528702
; GENERAL INFORMATION:
; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Tesfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RT2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
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; LENGTH: 165
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; ORGANISM: Brassica napus
US-09-519-232-56
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Query Match 5.3%; Score 7; DB 4; Length 165;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
| | | | |
Db 21 LDEANGL 27

RESULT 5

US-09-519-232-52
; Sequence 52, Application US/09519232
; Patent No. 6528702

GENERAL INFORMATION:

; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Testfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Brassica napus

US-09-519-232-52

Query Match 5.3%; Score 7; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
| | | | |
Db 21 LDEANGL 27

RESULT 6

US-09-519-232-54
; Sequence 54, Application US/09519232
; Patent No. 6528702

GENERAL INFORMATION:

; APPLICANT: Salmeron, John
; APPLICANT: Weislo, Laura
; APPLICANT: Willits, Michael
; APPLICANT: Mengiste, Testfaye
; TITLE OF INVENTION: NOVEL PLANT GENES AND USES THEREOF
; FILE REFERENCE: S-30857A/RTP2095
; CURRENT APPLICATION NUMBER: US/09/519,232
; CURRENT FILING DATE: 2000-03-06
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Brassica napus

US-09-519-232-54

Query Match 5.3%; Score 7; DB 4; Length 166;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
| | | | |
Db 21 LDEANGL 27

RESULT 7

US-09-270-767-58283
; Sequence 58283, Application US/09270767
; Patent No. 6703491

; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 58283
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Drosophila melanogaster

US-09-270-767-58283

Query Match 5.3%; Score 7; DB 4; Length 227;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 126 PCEVSVV 132
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Db 11 PCEVSVV 17

RESULT 8

US-09-134-000C-5641
; Sequence 5641, Application US/09134000C
; Patent No. 6617156

GENERAL INFORMATION:

; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5641
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Enterococcus faecalis

US-09-134-000C-5641

Query Match 5.3%; Score 7; DB 4; Length 231;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 GLDEESK 49
| | | | |
Db 175 GLDEESK 181

RESULT 9

US-09-393-634-55
; Sequence 55, Application US/09393634
; Patent No. 6558910

GENERAL INFORMATION:

; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliot
; APPLICANT: Ryba, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SP, a No. 6558910e1 Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 55
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human GR11
; NAME/KEY: MOD RES
; LOCATION: (1)-(245)
; OTHER INFORMATION: Xaa = any amino acid
US-09-393-634-55

Query Match          5.3%; Score 7; DB 4; Length 245;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 LLVSCPK 63
Db 150 LLVSCPK 156

RESULT 10
US-09-252-991A-24594
; Sequence 24594, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 24594
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-24594

Query Match          5.3%; Score 7; DB 4; Length 312;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 111 LDEANGL 117
Db 197 LDEANGL 203

RESULT 11
US-09-949-016-6081
; Sequence 6081, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6081
; LENGTH: 419
; TYPE: PRT
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; ORGANISM: Human
US-09-949-016-6081

Query Match          5.3%; Score 7; DB 4; Length 419;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 FSILNAK 78
Db 41 FSILNAK 47

RESULT 12
US-09-949-016-10720
; Sequence 10720, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10720
; LENGTH: 430
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10720

Query Match          5.3%; Score 7; DB 4; Length 430;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 FSILNAK 78
Db 51 FSILNAK 57

RESULT 13
US-09-538-092-1365
; Sequence 1365, Application US/09538092
; Patent No. 6753314
; GENERAL INFORMATION:
; APPLICANT: Giot, Loic
; APPLICANT: Mansfield, Traci A.
; TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
; FILE REFERENCE: 15966-542
; CURRENT APPLICATION NUMBER: US/09/538,092
; CURRENT FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: 60/127,352
; PRIOR FILING DATE: 1999-04-01
; PRIOR APPLICATION NUMBER: 60/178,965
; PRIOR FILING DATE: 2000-02-01
; NUMBER OF SEQ ID NOS: 1387
; SOFTWARE: CurapatSeqFormatter Version 0.9
; SEQ ID NO 1365
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: Polypeptide Accession Number Q92696
US-09-538-092-1365
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Query Match 5.3%; Score 7; DB 4; Length 567;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 CLRVNPK 42
| | | | |
Db 99 CLRVNPK 105

RESULT 14
US-09-583-110-5255
; Sequence 5255, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: Pneumoniae for Diagnostics and Therapeutics
; CURRENT APPLICATION NUMBER: US/09/583,110
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5255
; LENGTH: 684
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5255

Query Match 5.3%; Score 7; DB 4; Length 684;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 BESKDYL 52
| | | | |
Db 410 BESKDYL 416

RESULT 15
US-09-107-433-4260
; Sequence 4260, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGNOSTICS
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:

; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4260:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 691 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...691
; SEQUENCE DESCRIPTION: SEQ ID NO: 4260:
US-09-107-433-4260

Query Match 5.3%; Score 7; DB 4; Length 691;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 46 BESKDYL 52
| | | | |
Db 417 BESKDYL 423

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:37:15 ; Search time 99.45 Seconds
(without alignments)
787.814 Million cell updates/sec

Title: US-09-706-325-12

Perfect score: 153

Sequence: 1 FTSELVPSYDSATFVLENFS.....FQVRSPTFQKSRDQHWYIT 153

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Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	124	81.0	961	2	Q6PCX9
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23	7	4.6	255	2	Q74D44
24	7	4.6	257	2	Q9WXV4
25	7	4.6	261	2	Q70EC9
26	7	4.6	271	2	Q6REK7
27	7	4.6	278	2	Q7UEF2
28	7	4.6	280	2	Q8NQ59
29	7	4.6	285	2	Q9UZA2
30	7	4.6	307	2	Q87TD8
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33	7	4.6	319	2	Q8KJC1
34	7	4.6	320	2	Q98K82
35	7	4.6	320	2	Q81N26
36	7	4.6	320	2	Q6HG72
37	7	4.6	321	2	Q813B9
38	7	4.6	325	2	Q8BRB6
39	7	4.6	330	2	Q92N54
40	7	4.6	339	2	Q889P7
41	7	4.6	335	2	Q8R831
42	7	4.6	357	2	Q8NUC9
43	7	4.6	366	2	Q6A7R5
44	7	4.6	369	2	Q8G211
45	7	4.6	377	2	Q8YFW9
46	7	4.6	430	2	Q61PL4
47	7	4.6	433	2	Q7QBX7
48	7	4.6	441	2	Q9V792
49	7	4.6	444	2	Q86823
50	7	4.6	454	2	Q6CGZ2
51	7	4.6	493	2	Q6VUB6
52	7	4.6	496	2	Q8ERP3
53	7	4.6	504	2	Q6RJO6
54	7	4.6	505	2	Q61UV3
55	7	4.6	505	2	Q631B3
56	7	4.6	505	2	Q72XL8
57	7	4.6	505	2	Q815C6
58	7	4.6	505	2	Q81K57
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60	7	4.6	505	2	Q6HB48
61	7	4.6	507	2	Q929S7
62	7	4.6	507	2	Q71X82
63	7	4.6	507	2	Q9X4A5
64	7	4.6	509	2	Q7RX54
65	7	4.6	510	2	Q62RF3
66	7	4.6	510	2	Q7NQ38
67	7	4.6	512	1	OPUD_BACSU
68	7	4.6	512	2	Q65FZ6
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70	7	4.6	546	2	Q8CPC3
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72	7	4.6	548	2	Q931S4
73	7	4.6	548	2	Q99UC9
74	7	4.6	548	2	Q7A0Z0
75	7	4.6	548	2	Q6G9L0
76	7	4.6	548	2	Q6GH56
77	7	4.6	553	2	Q7PWV8
78	7	4.6	555	2	Q8BH92
79	7	4.6	555	2	Q8C3C6
80	7	4.6	555	2	Q8C3W8
81	7	4.6	579	2	Q6PBQ3
82	7	4.6	586	2	Q6ZPW4
83	7	4.6	617	2	Q64M08
84	7	4.6	620	2	Q813X9
85	7	4.6	633	2	Q753Y3
86	7	4.6	633	2	Q755J3
87	7	4.6	651	2	Q9H4F0
88	7	4.6	651	2	Q9NTV6
89	7	4.6	702	2	Q7MW63
90	7	4.6	705	2	Q7R282
91	7	4.6	727	2	Q9X1L9
92	7	4.6	769	2	Q6Z0U0
93	7	4.6	785	2	Q7ZVP1
94	7	4.6	801	2	Q7MZU4
95	7	4.6	818	2	Q9SLI6
96	7	4.6	851	2	Q7UJH3
97	7	4.6	851	2	Q7XUD5
98	7	4.6	890	2	Q48541
99	7	4.6	904	2	Q9FYI0
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101	7	4.6	962	2	Q9S7S8
102	7	4.6	1014	2	Q68JA2
103	7	4.6	1014	2	Q7WUD4
104	7	4.6	1044	2	Q70CT4

Q7t2h3	oncorhynch
Q8Kjc1	rhizobium 1
Q98k82	rhizobium 1
Q81n26	bacillus an
Q6hg72	bacillus th
Q813b9	bacillus ce
Q8brb6	mus musculu
Q92n54	rhizobium m
Q889p7	pseudomonas
Q8r831	thermoanaer
Q8nuc9	corynebacte
Q6a7r5	propionibac
Q8g211	brucella su
Q8yfw9	brucella me
Q61pl4	homo sapien
Q7qbx7	anopheles g
Q9v792	drosophila
Q86823	streptomyce
Q6cgz2	yarrowia li
Q6vub6	marinococcu
Q8erp3	oceanobacil
Q8rjq6	halobacillu
Q61uv3	halobacillu
Q631b3	bacillus ce
Q72xl8	bacillus ce
Q815c6	bacillus ce
Q81k57	bacillus an
Q8et62	oceanobacil
Q6hb48	bacillus th
Q929s7	listeria in
Q71x82	listeria mo
Q9x4a5	listeria mo
Q7rx54	neurospora
Q8zrf3	bacillus li
Q7nq38	chromobacte
P5417	bacillus su
Q65fz6	bacillus li
Q6vth4	marinococcu
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Q6pbq3	chlamydomon
Q6zpw4	mus musculu
Q64m08	bacteroides
Q813x9	bacillus ce
Q753y3	ashbya goss
Q755j3	ashbya goss
Q9h4f0	homo sapien
Q9nyv6	homo sapien
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Q9x1l9	arabidopsis
Q6z0u0	oryza sativ
Q7zvp1	brachydanio
Q7mzu4	photobacillu
Q9sl16	arabidopsis
Q7uhj3	rhodopirell
Q7xud5	oryza sativ
Q48541	hordeum vul
Q9fyi0	hordeum vul
Q8ik09	plasmodium
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Q7wud4	escherichia
Q70ct4	arabidopsis

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107	7	4.6	1351	2	Q8XZ58	Q8xz58 raistonia s	180	6	3.9	111	2	Q6NC40	Q6nc40 rhodopseudo
108	7	4.6	1369	2	Q6NZJ7	Q6nzj7 mus musculus	181	6	3.9	114	2	Q7QLA1	Q7qla1 anopheles g
109	7	4.6	1390	2	Q8TH66	Q8th66 dictyosteli	182	6	3.9	116	2	P90861	P90861 caenorhabdi
110	7	4.6	1515	2	Q96VK4	Q96vk4 emericella	183	6	3.9	116	2	Q9S9A4	Q9s9a4 vicia faba
111	7	4.6	1777	2	Q89278	Q89278 himetobi p	184	6	3.9	118	1	YDIL_ECOLI	P76196 escherichia
112	7	4.6	1777	2	Q8F3H3	Q8f3h3 himetobi p	185	6	3.9	118	1	YDIL_ECOLI	Q654k8 oryza sativ
113	7	4.6	2224	2	Q8F8Y4	Q8f8y4 xanthomonas	186	6	3.9	118	2	Q654K8	Q654k8 oryza sativ
114	7	4.6	3805	2	Q7YXLI	Q7yxl1 cryptospori	187	6	3.9	118	2	Q7UUAH2	Q7uah2 shigella fl
115	7	4.6	4578	2	Q42181	Q42181 fugu rubrip	188	6	3.9	118	2	Q80117	Q80117 petromyzon
116	7	4.6	13536	2	Q83VS0	Q83vs0 pseudomonas	189	6	3.9	119	2	Q6N539	Q6n539 rhodopseudo
117	6	3.9	31	2	Q76030	Q76030 homo sapien	190	6	3.9	119	2	Q8BXT4	Q8bxt4 mus musculu
118	6	3.9	38	2	Q7R6R2	Q7r6r2 giardia lam	191	6	3.9	120	2	Q7QZB7	Q7qzb7 giardia lam
119	6	3.9	38	2	Q44102	Q44102 rattus norv	192	6	3.9	120	2	Q94ES4	Q94es4 pisum sativ
120	6	3.9	40	2	Q33162	Q33162 methanoharc	193	6	3.9	120	2	Q729Y5	Q729ys desulfovibr
121	6	3.9	44	2	Q06684	Q06684 treponema d	194	6	3.9	121	2	Q9W218	Q9w218 drosophila
122	6	3.9	47	2	Q73198	Q73198 wolbachia p	195	6	3.9	121	2	Q6AAH7	Q6aah7 propionibac
123	6	3.9	50	2	Q6VEO9	Q6veq9 mycobacteri	196	6	3.9	121	2	Q6D2Q0	Q6d2q0 erwina car
124	6	3.9	54	2	Q75QM5	Q75qms bacterioph	197	6	3.9	124	2	Q86U47	Q86u47 homo sapien
125	6	3.9	54	2	Q75QM5	Q75qms bacterioph	197	6	3.9	124	2	Q86U47	Q86u47 homo sapien
126	6	3.9	56	2	Q70BF8	Q70bf8 borrelia ga	198	6	3.9	124	2	Q06566	Q06030 chlamydia s
127	6	3.9	58	2	Q6KAW2	Q6kaw2 pneumocysti	199	6	3.9	124	2	Q7U0M4	Q7u0m4 mycobacteri
128	6	3.9	61	2	Q72763	Q72763 homo sapien	200	6	3.9	124	2	Q6MDM6	Q6mdm6 parachlamyd
129	6	3.9	61	2	Q72763	Q72763 homo sapien	201	6	3.9	126	2	Q8TM09	Q8tm09 methanoearc
130	6	3.9	62	2	Q7Y3G0	Q7y3g0 streptococc	202	6	3.9	127	2	Q83KV9	Q83kv9 shigella fl
131	6	3.9	62	2	Q8ETGL	Q8etgl borrelia ga	203	6	3.9	127	2	Q8FH45	Q8fh45 escherichia
132	6	3.9	64	2	Q7RI30	Q7ri30 plasmodium	204	6	3.9	127	2	Q8X5Y6	Q8x5y6 escherichia
133	6	3.9	64	2	Q41403	Q41403 sesbania ro	205	6	3.9	129	2	Q929D4	Q929d4 listeria in
134	6	3.9	65	2	Q9F6C5	Q9f6c5 borrelia ga	206	6	3.9	129	2	Q82NH2	Q82nh2 streptomyce
135	6	3.9	65	2	Q41019	Q41019 paramecium	207	6	3.9	129	2	Q8BJX7	Q8bjx7 mus musculu
136	6	3.9	66	2	Q6RUP9	Q6rup9 homo sapien	208	6	3.9	130	2	Q29186	Q29186 archaeoglob
137	6	3.9	71	2	Q96W62	Q96w62 pneumocysti	209	6	3.9	130	2	Q7MM63	Q7mm63 vibrio vuln
138	6	3.9	71	2	Q96W63	Q96w63 pneumocysti	210	6	3.9	130	2	Q87NA2	Q87na2 vibrio para
139	6	3.9	71	2	Q96W64	Q96w64 pneumocysti	211	6	3.9	130	2	Q8D8A5	Q8d8a5 vibrio vuln
140	6	3.9	71	2	Q96W65	Q96w65 pneumocysti	212	6	3.9	130	2	Q9ACV7	Q9acv7 streptomyce
141	6	3.9	71	2	Q96W66	Q96w66 pneumocysti	213	6	3.9	131	2	Q8Q0T6	Q8q0t6 methanoearc
142	6	3.9	71	2	Q96W67	Q96w67 pneumocysti	214	6	3.9	131	2	Q8Y535	Q8y535 listeria mo
143	6	3.9	77	2	Q97W40	Q97w40 sulfolobus	215	6	3.9	131	2	Q71XC4	Q71xc4 listeria mo
144	6	3.9	79	2	Q9P935	Q9p935 clonostachy	216	6	3.9	132	2	Q82L93	Q82l93 streptomyce
145	6	3.9	80	2	Q6Z1J5	Q6z1j5 oryza sativ	217	6	3.9	132	2	Q89BQ1	Q89bq1 bradyrhizob
146	6	3.9	81	2	Q9XGV1	Q9xgv1 lycopersico	218	6	3.9	133	1	Y843_AQUAE	Q67011 aquifex aeo
147	6	3.9	83	2	Q7MJAT	Q7mja7 vibrio vuln	219	6	3.9	134	2	Q9LT36	Q9lt36 arabidopsis
148	6	3.9	83	2	Q7MNE2	Q7mb2 vibrio vuln	220	6	3.9	135	2	Q7PIM0	Q7pin0 anopheles g
149	6	3.9	84	2	Q671S6	Q671s6 oryza sativ	221	6	3.9	135	2	Q9FC41	Q9fc41 streptomyce
150	6	3.9	85	2	Q7RM06	Q7rm06 plasmodium	222	6	3.9	136	2	Q9XFD2	Q9xfid2 oryza sativ
151	6	3.9	85	2	Q9XHG3	Q9xhg3 arabidopsis	223	6	3.9	136	2	Q54938	Q54938 ondatra zib
152	6	3.9	86	2	Q49969	Q49969 solanum tub	224	6	3.9	137	2	Q94ES3	Q94es3 pisum sativ
153	6	3.9	86	2	Q6VER6	Q6ver6 mycobacteri	225	6	3.9	138	2	Q729E0	Q729e0 desulfovibr
154	6	3.9	86	2	Q9F6K6	Q9f6k6 borrelia ga	226	6	3.9	141	2	Q6L2B3	Q6l2b3 methanococc
155	6	3.9	87	2	Q8FBH7	Q8fbh7 brachydanio	227	6	3.9	141	2	Q9Y244	Q9y244 homo sapien
156	6	3.9	89	2	Q911T3	Q911t3 pseudomonas	228	6	3.9	141	2	Q7QZP8	Q7qzpb giardia lam
157	6	3.9	90	2	Q709R9	Q709r9 human immun	229	6	3.9	141	2	Q9CXV8	Q9cxv8 mus musculu
158	6	3.9	94	2	Q9RJN0	Q9rjn0 streptomyce	230	6	3.9	141	2	Q9CZL7	Q9czl7 mus musculu
159	6	3.9	97	2	Q87GH3	Q87gh3 vibrio para	231	6	3.9	141	2	Q9COT5	Q9cot5 m mus muscu
160	6	3.9	97	2	Q8E3A3	Q8e3a3 streptococc	232	6	3.9	142	2	Q8PTQ2	Q8ptq2 methanoearc
161	6	3.9	98	2	Q24186	Q24186 oryza sativ	233	6	3.9	142	2	Q67UQ6	Q67ud6 oryza sativ
162	6	3.9	98	2	Q8H317	Q8h317 oryza sativ	234	6	3.9	142	2	Q8KGS7	Q8kgs7 chlorobium
163	6	3.9	98	2	Q6AQ57	Q6aq57 desulfofale	235	6	3.9	142	2	Q67625	Q67625 melesgrid h
164	6	3.9	101	2	Q49968	Q49968 solanum tub	236	6	3.9	143	2	Q6ZQ80	Q6zq80 homo sapien
165	6	3.9	101	2	Q81UH7	Q81uh7 bacillus an	237	6	3.9	144	2	Q08439	Q08439 saccharomyc
166	6	3.9	102	1	RS10_TREDE	Q73pn2 treponema d	238	6	3.9	144	2	Q08ABF9	Q08abf9 bacteroides
167	6	3.9	102	1	RS10_TREPA	Q83218 treponema p	239	6	3.9	145	2	Q8KNP6	Q8knp6 bacillus th
168	6	3.9	102	2	Q14278	Q14278 homo sapien	240	6	3.9	146	2	Q68V63	Q68v63 uncultured
169	6	3.9	102	2	Q811X0	Q811x0 plasmodium	241	6	3.9	146	2	Q68V64	Q68v64 uncultured
170	6	3.9	105	2	Q6MY55	Q6mys5 aspergillus	242	6	3.9	146	2	Q68V66	Q68v66 uncultured
171	6	3.9	105	2	Q6AP72	Q6ap72 desulfofale	243	6	3.9	146	2	Q68V67	Q68v67 uncultured
172	6	3.9	106	2	Q89S46	Q89s46 bradyrhizob	244	6	3.9	146	2	Q68V68	Q68v68 uncultured
173	6	3.9	108	2	Q63FB0	Q63fb0 bacillus ce	245	6	3.9	146	2	Q68V72	Q68v72 uncultured
174	6	3.9	108	2	Q73CT3	Q73ct3 bacillus ce	246	6	3.9	146	2	Q68V73	Q68v73 uncultured
175	6	3.9	108	2	Q6HMT4	Q6hmt4 bacillus th	247	6	3.9	146	2	Q68V79	Q68v79 uncultured
176	6	3.9	109	2	Q6YXJ4	Q6yxj4 oryza sativ	248	6	3.9	146	2	Q68V80	Q68v80 uncultured
177	6	3.9	109	2	Q81HB7	Q81hb7 bacillus ce	249	6	3.9	147	2	Q93NF3	Q93nf3 arthrobacte
							250	6	3.9				

251	6	3.9	147	2	Q2M26	Q92m26 rhizobium m	324	6	3.9	188	2	O30134	O30134 archaeoglob
252	6	3.9	147	2	Q237P5	Q737p5 bacillus ce	325	6	3.9	188	2	P73277	P73277 synechocyst
253	6	3.9	148	2	Q22500	Q22500 caenorhabdi	326	6	3.9	188	2	O9JL38	O9JL38 mus musculus
254	6	3.9	149	1	Y2801 LEIXX	Q6ah32 leifsonia x	327	6	3.9	189	2	O74323	O74323 e signal pe
255	6	3.9	149	2	Q89012	Q89012 lactobacilli	328	6	3.9	189	2	O8A356	O8A356 bacteroides
256	6	3.9	150	2	Q66086	Q66086 canine herp	329	6	3.9	189	2	O9PCH8	O9PCH8 xylella fas
257	6	3.9	152	2	Q9MFC5	Q9mfc5 beta vulgar	330	6	3.9	190	1	CYGB_HUMAN	Q8wmm9 homo sapien
258	6	3.9	153	2	Q64A10	Q64a10 uncultured	331	6	3.9	190	2	O8N2X5	Q8n2x5 homo sapien
259	6	3.9	153	2	O8YJQ9	O8Yjg9 brucella me	332	6	3.9	190	2	O8GHN3	O8ghn3 pseudomonas
260	6	3.9	154	2	O7M127	Q7mlz7 daucus caro	333	6	3.9	191	1	PTH_MYCBO	P65866 mycobacteri
261	6	3.9	154	2	Q7XZ67	Q7xz67 griffithsia	334	6	3.9	191	1	PTH_MYCTU	P65865 mycobacteri
262	6	3.9	155	2	Q7VP20	Q7vp20 haemophilus	335	6	3.9	191	2	Q741V9	Q741v9 mycobacteri
263	6	3.9	157	2	Q8DXN3	Q8dxn3 streptococc	336	6	3.9	193	1	YN42_CAUCR	Q9a5v5 caulobacter
264	6	3.9	158	2	Q8XQL8	Q8xql8 ralsstonia s	337	6	3.9	193	2	O9NX89	Q9nx89 homo sapien
265	6	3.9	158	2	Q7VL01	Q7vl01 haemophilus	338	6	3.9	194	2	O66080	Q66080 canine herp
266	6	3.9	159	2	P73640	P73640 synechocyst	339	6	3.9	195	2	O9NAJ1	Q9naj1 caenorhabdi
267	6	3.9	160	2	Q7N1H1	Q7nlh1 photorhabdu	340	6	3.9	196	2	Q9VAA1	Q9vaa1 drosophila
268	6	3.9	161	1	Ru11_METWA	Q9py53 methanosarc	341	6	3.9	196	2	O6FDU6	Q6fdu6 acinetobact
269	6	3.9	161	2	Q8U4L4	Q8u4l4 pyrococcus	342	6	3.9	196	2	O83D18	Q83d18 coxiella bu
270	6	3.9	161	2	Q9HB69	Q9hb69 homo sapien	343	6	3.9	197	2	O9VZ32	Q9vz32 drosophila
271	6	3.9	161	2	O32085	O32085 bacillus su	344	6	3.9	198	2	O7RYR1	O7ryr1 neurospora
272	6	3.9	161	2	O7ME07	Q7me07 vibrio vuln	345	6	3.9	198	2	O6YV95	O6yv95 oryza sativ
273	6	3.9	161	2	Q7WE75	Q7we75 bordetella	346	6	3.9	199	1	PTH_MYCLE	Q9cd49 mycobacteri
274	6	3.9	161	2	Q6S9W2	Q6s9w2 columbid ci	347	6	3.9	199	2	O6EN01	Q6en01 trimeresuru
275	6	3.9	162	2	Q64EG2	Q64eg2 uncultured	348	6	3.9	199	2	O8PA66	Q8pa66 xanthomonas
276	6	3.9	162	2	O87Z67	Q87z67 pseudomonas	349	6	3.9	200	2	O9PX32	Q9px32 human herpe
277	6	3.9	164	2	O05127	O05127 neisseria g	350	6	3.9	200	2	O9W8K2	Q9w8k2 human herpe
278	6	3.9	171	2	O98LE9	Q98le9 rhizobium l	351	6	3.9	200	2	O9YUA9	O9yua9 human immun
279	6	3.9	165	2	Q747H7	Q747h7 geobacter s	352	6	3.9	201	2	Q7QNV9	Q7qnv9 giardia lam
280	6	3.9	166	2	Q6XND3	Q6xnd3 rhodococcus	353	6	3.9	201	2	Q7YXH2	Q7yxh2 caenorhabdi
281	6	3.9	171	1	YCBV_ECOLI	P75860 escherichia	354	6	3.9	202	2	O6VOM5	Q6vom5 mycobacteri
282	6	3.9	171	2	O9PHF9	Q9phf9 xanthomonas	355	6	3.9	203	2	O9KMZ7	Q9kmz7 vibrio chol
283	6	3.9	171	2	O82N41	Q82n41 streptomyce	356	6	3.9	204	2	O9RC46	Q9rc46 bacillus ha
284	6	3.9	172	2	Q87CK2	Q87ck2 xylella fas	357	6	3.9	204	2	O98HN0	Q98hn0 rhizobium l
285	6	3.9	172	2	Q912Q0	Q912q0 pseudomonas	358	6	3.9	205	2	Q8ID59	Q8id59 plasmodium
286	6	3.9	175	2	Q84R71	Q84r71 oryza sativ	359	6	3.9	205	2	O9HZD9	Q9hzd9 pseudomonas
287	6	3.9	177	2	Q8IRP2	Q8irp2 drosophila	360	6	3.9	206	1	YX59_PSESM	Q87zr5 pseudomonas
288	6	3.9	178	2	Q82Y10	Q82y10 pyrobaculum	361	6	3.9	206	2	O74N80	Q74n80 nanoarchaeu
289	6	3.9	178	2	O97051	Q97051 pseudocardi	362	6	3.9	206	2	O7PIX6	Q7pix6 anopheles g
290	6	3.9	178	2	O87568	Q87568 helicobacte	363	6	3.9	206	2	O86EJ3	Q86ej3 schistosoma
291	6	3.9	178	2	Q8CR33	Q8cr33 staphylococ	364	6	3.9	206	2	Q8BRQ1	Q8brq1 mus musculus
292	6	3.9	178	2	Q9A5S1	Q9a5s1 caulobacter	365	6	3.9	208	1	Y4B5_PSEPK	Q88fr8 pseudomonas
293	6	3.9	179	2	Q7QIN0	Q7qin0 anopheles g	366	6	3.9	208	2	O8H014	Q8h014 oryza sativ
294	6	3.9	179	2	O8KW25	Q8kw25 ruegeria sp	367	6	3.9	208	2	O8YHJ5	Q8yhj5 brucella me
295	6	3.9	179	2	O87VNO	Q87vn0 pseudomonas	368	6	3.9	209	1	GEMI_HUMAN	O75496 homo sapien
296	6	3.9	179	2	Q88HE4	Q88he4 pseudomonas	369	6	3.9	211	2	O8BSI3	Q8bsi3 mus musculus
297	6	3.9	179	2	Q9QUC6	Q9quc6 tt virus..o	370	6	3.9	212	2	O9C9K9	Q9c9k9 arabidopsis
298	6	3.9	180	2	O50971	Q50971 neisseria g	371	6	3.9	212	2	O85372	O85372 rhodococcus
299	6	3.9	180	2	O8G0B3	Q8g0b3 brucella su	372	6	3.9	212	2	O83V10	Q83v10 corynebacte
300	6	3.9	181	2	O74KA6	Q74ka6 lactobacilli	373	6	3.9	213	2	O65EP8	O65ef8 bacillus li
301	6	3.9	181	2	O7DD77	Q7dd77 neisseria m	374	6	3.9	213	2	O7UMS1	O7umel rhodopirell
302	6	3.9	181	2	Q9JQK6	Q9jqk6 neisseria m	375	6	3.9	214	2	O7Q2M4	Q7q2m4 anopheles g
303	6	3.9	182	2	O04410	O04410 raphanus sa	376	6	3.9	214	2	O657Y6	O657y6 oryza sativ
304	6	3.9	182	2	Q6RVZ1	Q6rvz1 bifidobacte	377	6	3.9	215	1	RPB5_CANGA	Q6fqa6 candida gla
305	6	3.9	182	2	Q8DXJ9	Q8dxj9 synechococc	378	6	3.9	215	1	RPB5_YEAST	P20434 saccharomyc
306	6	3.9	183	1	DIN1_RAPSA	P27626 raphanus sa	379	6	3.9	215	2	O9XEX0	Q9xex0 gracillaria
307	6	3.9	183	2	Q21131	Q21131 caenorhabdi	380	6	3.9	215	2	O8X4E4	O8x4e4 escherichia
308	6	3.9	183	2	Q9HXU2	Q9hxu2 pseudomonas	381	6	3.9	217	2	Q72A59	Q72a59 desulfovibr
309	6	3.9	184	2	Q9JF87	Q9jfr8 human immun	382	6	3.9	218	1	YD12_MYCPN	P75469 mycoplasma
310	6	3.9	185	2	Q9A357	Q9a357 bacteroides	383	6	3.9	218	2	O75A56	Q75a56 ashbya goes
311	6	3.9	186	1	RRF_RHOA	Q7uth0 rhodopirell	384	6	3.9	219	2	O9AS64	O9as64 oryza sativ
312	6	3.9	186	1	TNR5_PSEAE	P06692 escherichia	385	6	3.9	222	2	O75AR6	O75ar6 ashbya goes
313	6	3.9	186	1	TNR7_ECOLI	P06692 escherichia	386	6	3.9	222	2	O7WGT6	O7wgt6 bordetella
314	6	3.9	186	2	O66046	O66046 pseudomonas	387	6	3.9	223	2	O972K5	Q972k5 sulfolobus
315	6	3.9	186	2	Q934S3	Q934s3 thiobacilli	388	6	3.9	223	2	O64RB3	O64rb3 bacteroides
316	6	3.9	186	2	Q68E60	Q68e60 aeromonas p	389	6	3.9	223	2	O7VTZ4	O7vtz4 bordetella
317	6	3.9	186	2	Q7AXT9	Q7axt9 pseudomonas	390	6	3.9	223	2	O7WK92	O7wk92 bordetella
318	6	3.9	186	2	O7BE17	O7be17 shigella fl	391	6	3.9	224	2	O82M30	Q82m30 streptomyce
319	6	3.9	186	2	O9AJD0	O9ajd0 pseudomonas	392	6	3.9	224	2	O9RU88	Q9ru88 deinococcus
320	6	3.9	186	2	Q65IT1	Q65it1 bacillus li	393	6	3.9	225	2	O9ZBV3	Q9zbv3 streptomyce
321	6	3.9	187	2	Q7AG38	Q7ag38 escherichia	394	6	3.9	226	2	O9C828	Q9c828 arabidopsis
322	6	3.9	187	2	O8X581	Q8x581 escherichia	395	6	3.9	226	2	O33188	O33188 mycobacteri
323	6	3.9	187	2	O83RX8	Q83rx8 shigella fl	396	6	3.9	226	2	O7TZS6	O7tzes6 mycobacteri

397	6	3.9	227	2	Q6C587	Q6c587 yarrowia li	470	6	3.9	252	2	Q8RH62	Q8rh62 fusobacteri
398	6	3.9	227	2	Q7MUR2	Q7mur2 porphyromon	471	6	3.9	253	2	Q97YU2	Q97yu2 sulfolobus
399	6	3.9	227	2	Q9RWX2	Q9rxw2 deinococcus	472	6	3.9	253	2	Q70MM8	Q70mm8 crassostrea
400	6	3.9	230	1	AQP2_PSEPK	Q88f17 pseudomonas	473	6	3.9	254	2	Q9UF65	Q9uf65 homo sapien
401	6	3.9	230	1	UL16_HCMVA	P16757 human cytom	474	6	3.9	255	2	P78727	P78727 pneumocysti
402	6	3.9	230	2	Q8H6CO	Q8h6c0 silene lati	475	6	3.9	255	2	Q6NLM6	Q6nlm6 drosophila
403	6	3.9	230	2	Q7M6R7	Q7m6r7 human cytom	476	6	3.9	255	2	Q68049	Q68049 rhodobacter
404	6	3.9	230	2	Q7TF85	Q7tf85 human cytom	477	6	3.9	255	2	Q88NR7	Q88nr7 pseudomonas
405	6	3.9	231	2	Q67SV4	Q67sv4 symbiobacte	478	6	3.9	256	2	Q9P856	Q9p856 trypanosoma
406	6	3.9	232	2	Q9LAS2	Q9las2 desulfitoba	479	6	3.9	256	2	Q7P856	Q7pe86 atopheles g
407	6	3.9	232	2	Q8ZN09	Q8zn09 salmonella	480	6	3.9	256	2	Q9DXV5	Q9dxv5 tomato spot
408	6	3.9	232	2	Q74I11	Q74i11 lactobacill	481	6	3.9	257	1	DLHH_SULSO	P95862 sulfolobus
409	6	3.9	233	2	P78728	P78728 pneumocysti	482	6	3.9	258	2	Q8FY43	Q8fy43 brucella su
410	6	3.9	233	2	P78730	P78730 pneumocysti	483	6	3.9	259	2	Q92KZ5	Q92kz5 rhizobium m
411	6	3.9	233	2	Q6TLZ5	Q6tlz5 mycobacteri	484	6	3.9	260	2	Q6BQC2	Q6bqc2 debaryomyce
412	6	3.9	233	2	Q92Z40	Q92z40 rhizobium m	485	6	3.9	260	2	Q7VM79	Q7vm79 haemophilus
413	6	3.9	233	2	Q7NGN2	Q7ngn2 gloeobacter	486	6	3.9	261	2	Q96XK4	Q96xk4 sulfolobus
414	6	3.9	233	2	Q9JV64	Q9jv64 neisseria m	487	6	3.9	261	2	P78729	P78729 pneumocysti
415	6	3.9	233	2	Q9K054	Q9k054 neisseria m	488	6	3.9	261	2	Q94YM6	Q94ym6 rana nigrom
416	6	3.9	234	1	SNG1_HUMAN	Q83759 homo sapien	489	6	3.9	261	2	Q6L7I1	Q6l7i1 buergeria b
417	6	3.9	234	1	SNG1_MOUSE	Q5100 mus musculu	490	6	3.9	261	2	Q98CP4	Q98cp4 thizobium l
418	6	3.9	234	1	SNG1_RAT	Q62876 rattus norv	491	6	3.9	261	2	Q7V5J8	Q7v5j8 bordetella
419	6	3.9	234	2	Q26747	Q26747 methanobact	492	6	3.9	261	2	Q7W459	Q7w459 bordetella
420	6	3.9	235	2	Q662B2	Q662e2 borrelia ga	493	6	3.9	261	2	Q7WFL6	Q7wfl6 bordetella
421	6	3.9	235	2	Q92KY7	Q92ky7 rhizobium m	494	6	3.9	262	2	Q9RB26	Q9rb26 pectobacter
422	6	3.9	236	2	Q8ZWR9	Q8zwr9 pyrobaculum	495	6	3.9	262	2	Q9XB51	Q9xb51 erwinia car
423	6	3.9	236	2	Q82ZB2	Q82zb2 enterococcu	496	6	3.9	262	2	Q6CZM8	Q6czm8 erwinia car
424	6	3.9	239	2	Q987U4	Q987u4 rhizobium l	497	6	3.9	263	2	Q6CNJH0	Q6cnjh0 corynebacte
425	6	3.9	239	2	Q8D2M8	Q8d2m8 wiggleswort	498	6	3.9	264	2	Q87202	Q87202 azospirillu
426	6	3.9	239	2	Q9KFK5	Q9kfk5 bacillus ha	499	6	3.9	264	2	Q9HZV7	Q9hzv7 pseudomonas
427	6	3.9	240	2	Q30144	Q30144 archaeoglob	500	6	3.9	264	2	Q7QQF8	Q7qqf8 giardia lam
428	6	3.9	240	2	Q6NCC7	Q6ncc7 rhodopseudo	501	6	3.9	265	2	Q8RPD5	Q8rpd5 legionella
429	6	3.9	241	2	Q6FPW6	Q6fpw6 candida gla	502	6	3.9	265	2	Q9FDK8	Q9fdk8 zymomonas m
430	6	3.9	242	2	Q81JV6	Q81jv6 plasmod.um	503	6	3.9	265	2	Q7V3Z4	Q7v3z4 prochloroco
431	6	3.9	242	2	Q7Z0H0	Q7z0h0 plasmod.um	504	6	3.9	266	2	Q7VNX0	Q7vnx0 haemophilus
432	6	3.9	242	2	Q82RL6	Q82rl6 streptonyce	505	6	3.9	266	2	Q6DCS4	Q6dcs4 brachydanio
433	6	3.9	242	2	Q6AKI2	Q6aki2 desulfotale	506	6	3.9	267	2	Q6CLX9	Q6clx9 kluyveromyc
434	6	3.9	242	2	Q8BF77	Q8bf77 uncultured	507	6	3.9	268	1	ET1B_XENLA	P18756 xenopus lae
435	6	3.9	242	2	Q6RXJ0	Q6rxj0 human cytom	508	6	3.9	268	2	Q8I6J7	Q8i6j7 ciona intes
436	6	3.9	242	2	Q75RX5	Q75rx5 oreochromis	509	6	3.9	269	2	Q9W4X7	Q9w4x7 drosophila
437	6	3.9	243	2	Q6INE4	Q6ine4 xenopus lae	510	6	3.9	269	2	Q74PA9	Q74pa9 yersinia pe
438	6	3.9	244	2	Q8WQV9	Q8wqv9 aphroca.lis	511	6	3.9	269	2	Q8YBG1	Q8ybg1 brucella me
439	6	3.9	244	2	Q74K22	Q74k22 lactobacill	512	6	3.9	269	2	Q89FH2	Q89fh2 bradyrhizob
440	6	3.9	245	2	Q8Y1B9	Q8y1b9 raietsonia s	513	6	3.9	269	2	Q8CFZ9	Q8cfz9 yersinia pe
441	6	3.9	245	2	Q88I43	Q88i43 pseudomonas	514	6	3.9	269	2	Q8FWY4	Q8fwy4 brucella su
442	6	3.9	246	2	Q6IWO4	Q6iwo4 burkholderi	515	6	3.9	270	2	Q74DN6	Q74dn6 geobacter s
443	6	3.9	246	2	Q9SY37	Q9sy37 arabidopsis	516	6	3.9	271	2	P78731	P78731 pneumocysti
444	6	3.9	246	2	Q6NGB2	Q6ngb2 fusobacteri	517	6	3.9	272	2	Q97L38	Q97l38 clostridium
445	6	3.9	246	2	Q6NGD2	Q6ngd2 corynebacte	518	6	3.9	273	2	Q91G96	Q91g96 columbid ci
446	6	3.9	246	2	Q7NFW3	Q7nfw3 gloeobacter	519	6	3.9	273	2	Q91GA1	Q91ga1 columbid ci
447	6	3.9	247	1	Y125_RICPR	P41087 rickettsia	520	6	3.9	273	2	Q91G42	Q91g42 columbid ci
448	6	3.9	247	1	Y167_RICCN	Q92ja0 rickettsia	521	6	3.9	274	1	GADX_ECO27	GADX_ECO27
449	6	3.9	247	2	Q7PAR7	Q7par7 rickettsia	522	6	3.9	274	1	GADX_ECO57	GADX_ECO57
450	6	3.9	247	2	Q8PPL6	Q8ppl6 xanthomonas	523	6	3.9	274	1	GADX_ECOL6	GADX_ECOL6
451	6	3.9	247	2	Q68XP2	Q68xp2 rickettsia	524	6	3.9	274	1	GADX_ECOLI	GADX_ECOLI
452	6	3.9	247	2	Q9KFL0	Q9kfl0 bacillus ha	525	6	3.9	274	1	GADX_SHIFL	GADX_SHIFL
453	6	3.9	247	2	Q8BF96	Q8bf96 uncultured	526	6	3.9	274	1	THCF_RHOER	THCF_RHOER
454	6	3.9	248	1	GRPE_ANASP	P95438 pseudomonas	527	6	3.9	275	2	Q9A3U3	Q9a3u3 caulobacter
455	6	3.9	248	2	P95438	Q9yua7 anabaena sp	528	6	3.9	275	2	Q6ML97	Q6ml97 bdellovibri
456	6	3.9	248	2	Q73ECO	Q73eco bacillus ce	529	6	3.9	275	2	Q9CCW0	Q9ccw0 mycobacteri
457	6	3.9	248	2	Q91314	Q91314 pseudomonas	530	6	3.9	276	2	Q6Z9X5	Q6z9x5 oryza sativ
458	6	3.9	249	2	Q6D4F3	Q6d4p3 erwinia car	531	6	3.9	276	2	Q737L6	Q737l6 bacillus ce
459	6	3.9	249	2	Q8UJ80	Q8uj80 agrobacteri	532	6	3.9	277	2	Q86ZC6	Q86zc6 gibberella
460	6	3.9	250	2	Q9LTG7	Q9ltg7 arabidopsis	533	6	3.9	277	2	Q53640	Q53640 streptococc
461	6	3.9	250	2	Q636V7	Q636v7 bacillus ce	534	6	3.9	277	2	Q887P6	Q887p6 pseudomonas
462	6	3.9	250	2	Q8YMY8	Q8ymv8 anabaena sp	535	6	3.9	277	2	Q8DYF6	Q8dyf6 streptococc
463	6	3.9	250	2	Q733B4	Q733b4 bacillus ce	536	6	3.9	277	2	Q8DZN3	Q8dzn3 streptococc
464	6	3.9	250	2	Q81A69	Q81a69 bacillus ce	537	6	3.9	278	2	Q8FPY2	Q8fpy2 corynebacte
465	6	3.9	250	2	Q81W66	Q81w66 bacillus an	538	6	3.9	278	1	BMRR_BACSU	P39075 bacillus su
466	6	3.9	250	2	Q6HF92	Q6hf92 bacillus th	539	6	3.9	278	2	O64773	O64773 arabidopsis
467	6	3.9	251	2	Q663S0	Q663s0 yersinia ps	540	6	3.9	278	2	Q40768	Q40768 prunus dulc
468	6	3.9	251	2	Q8Z9T6	Q8z9t6 yersinia pe	541	6	3.9	280	2	Q8PI45	Q8pi45 xanthomonas
469	6	3.9	252	2	Q7P501	Q7p501 fusobacteri	542	6	3.9	281	2	Q64NUL1	Q64nul1 bacteroides

543	Q8TJZ1	methanosaarc	616	6	3.9	282	2	Q8TJZ1
544	Q74BQ6	gobacter s	617	6	3.9	282	2	Q74BQ6
545	P47148	saccharomyc	618	6	3.9	283	1	YJ81_YEAST
546	Q9AA26	caulobacter	619	6	3.9	283	2	Q9AA26
547	Q97UF4	sulfolobus	620	6	3.9	285	2	Q97UF4
548	Q53710	mycobacteri	621	6	3.9	286	2	Q53710
549	Q7U252	mycobacteri	622	6	3.9	286	2	Q7U252
550	Q9K706	caecilius ha	623	6	3.9	286	2	Q9K706
551	Q6TMV7	hyphomonas	624	6	3.9	287	2	Q6TMV7
552	Q8PMB7	xanthomonas	625	6	3.9	287	2	Q8PMB7
553	Q9CHQ9	lactococcus	626	6	3.9	287	2	Q9CHQ9
554	Q6DFO	xenopus tro	627	6	3.9	287	2	Q6DFO
555	Q6CVR6	kluyveromyc	628	6	3.9	288	2	Q6CVR6
556	Q9XU24	caenorhabdi	629	6	3.9	288	2	Q9XU24
557	Q8YSU1	naabaena sp	630	6	3.9	289	2	Q8YSU1
558	Q9J5E0	fowlpox vir	631	6	3.9	289	2	Q9J5E0
559	EXOS_BPT5	P06229 bacteri	632	6	3.9	290	1	EXOS_BPT5
560	Y620_METJA	methanococc	633	6	3.9	291	1	Y620_METJA
561	Q97116	clostridium	634	6	3.9	291	2	Q97116
562	Q9RGM3	acinobact	635	6	3.9	292	1	MDCB_ACICA
563	Q8LAG0	arabidopsis	636	6	3.9	292	2	Q8LAG0
564	Q9FWT1	arabidopsis	637	6	3.9	292	2	Q9FWT1
565	Q9FY94	arabidopsis	638	6	3.9	292	2	Q9FY94
566	YFIE_ECOLI	P33634 escherichia	639	6	3.9	293	1	YFIE_ECOLI
567	Q72JW2	thermus the	640	6	3.9	293	2	Q72JW2
568	Q94E53	oryza sativ	641	6	3.9	294	2	Q94E53
569	Q9FWZ3	arabidopsis	642	6	3.9	294	2	Q9FWZ3
570	Q8P7C3	xanthomonas	643	6	3.9	294	2	Q8P7C3
571	Q8P1P6	xanthomonas	644	6	3.9	295	2	Q8P1P6
572	Q20811	caenorhabdi	645	6	3.9	295	2	Q20811
573	Q8PAE8	xanthomonas	646	6	3.9	295	2	Q8PAE8
574	MALG_ECOLI	escherichia	647	6	3.9	296	1	MALG_ECOLI
575	MALG_ECOLI	escherichia	648	6	3.9	296	1	MALG_ECOLI
576	MALG_ENTAB	escherichia	649	6	3.9	296	1	MALG_ENTAB
577	MALG_PHOLI	photobact	650	6	3.9	296	1	MALG_PHOLI
578	MALG_SALTI	salmonella	651	6	3.9	296	1	MALG_SALTI
579	MALG_SALTY	salmonella	652	6	3.9	296	1	MALG_SALTY
580	MALG_SHIFL	shigella fl	653	6	3.9	296	1	MALG_SHIFL
581	Q6CD51	yarowia li	654	6	3.9	296	1	Q6CD51
582	Q664X1	yersinia ps	655	6	3.9	296	2	Q664X1
583	Q7VIG3	helicobacte	656	6	3.9	297	2	Q7VIG3
584	Q9A589	caulobacter	657	6	3.9	297	2	Q9A589
585	Q8HX00	pseudomonas	658	6	3.9	297	2	Q8HX00
586	Q8QXV0	garlic late	659	6	3.9	297	2	Q8QXV0
587	Q8UZA2	garlic late	660	6	3.9	297	2	Q8UZA2
588	Q8X121	pneumocysti	661	6	3.9	298	2	Q8X121
589	Q8ZMX6	salmonella	662	6	3.9	298	2	Q8ZMX6
590	Q7MR96	wolinella s	663	6	3.9	299	2	Q7MR96
591	Q9VDJ3	drosophila	664	6	3.9	299	2	Q9VDJ3
592	Q7D9X3	mycobacteri	665	6	3.9	300	2	Q7D9X3
593	P96811	mycobacteri	666	6	3.9	300	2	P96811
594	Q6ARY6	desulfotale	667	6	3.9	300	2	Q6ARY6
595	Q9E7N7	lettuce nec	668	6	3.9	300	2	Q9E7N7
596	Q26437	methanobact	669	6	3.9	301	2	Q26437
597	Q65H73	caecilius li	670	6	3.9	301	2	Q65H73
598	Q85H73	brachydanio	671	6	3.9	301	2	Q85H73
599	Q9PPG1	bradyrhizob	672	6	3.9	301	2	Q9PPG1
600	Q74RF8	yersinia pe	673	6	3.9	303	1	MALG_YERPE
601	Q6EUG3	oryza sativ	674	6	3.9	303	2	Q6EUG3
602	Q8PLN1	xanthomonas	675	6	3.9	303	2	Q8PLN1
603	Q8K3X5	streptomyce	676	6	3.9	303	2	Q8K3X5
604	Q7Z663	brachydanio	677	6	3.9	303	2	Q7Z663
605	Q7V516	prochloroco	678	6	3.9	304	1	ASPA_PROMM
606	Q8BKX6	caenorhabdi	679	6	3.9	304	2	Q8BKX6
607	Q8EIN6	shewanella	680	6	3.9	304	2	Q8EIN6
608	Q9PJ28	campylobact	681	6	3.9	305	1	FMT_CAMJE
609	P72579	sulfolobus	682	6	3.9	305	2	P72579
610	Q96Y68	sulfolobus	683	6	3.9	305	2	Q96Y68
611	Q32796	lactococcus	684	6	3.9	305	2	Q32796
612	Q32798	lactococcus	685	6	3.9	305	2	Q32798
613	Q7ND98	gloeobacter	686	6	3.9	305	2	Q7ND98
614	Q835V5	enterococcu	687	6	3.9	305	2	Q835V5
615	Q91259	streptomyce	688	6	3.9	305	2	Q91259

P06599	daucus caro	306	1	EXTN DAUCA
P23311	saccharomyc	307	1	YMC1_YEAST
Q61QC7	brachydanio	307	2	Q61QC7
Q8FF12	escherichia	308	2	Q8FF12
Q83Q11	shigella fl	308	2	Q83Q11
Q8X5A8	escherichia	308	2	Q8X5A8
Q96EJ8	homo sapien	309	2	Q96EJ8
Q86X20	homo sapien	309	2	Q86X20
Q7MP27	vibrio vuln	309	2	Q7MP27
Q7N0A8	photobact	309	2	Q7N0A8
P16925	tetrathymena	310	1	CNJC_TETHH
P96562	amycolotops	310	2	P96562
P94984	caenorhabdi	311	2	O44984
Q87U08	pseudomonas	311	2	Q87U08
Q26631	methanobact	312	1	Y531_METTH
Q8Y711	listeria mo	312	2	Q8Y711
Q720F6	listeria mo	312	2	Q720F6
Q89588	clostridium	312	2	Q89588
Q6CLN0	kluyveromyc	313	2	Q6CLN0
Q25523	helicobacte	313	2	Q25523
Q8Y556	listeria mo	313	2	Q8Y556
Q71XE5	listeria mo	313	2	Q71XE5
Q8KA02	bacillus ha	313	2	Q8KA02
Q8ZKZ4	helicobacte	313	2	Q8ZKZ4
Q8YJ00	brucella me	314	1	HEM3_BRUMU
Q8FY16	brucella su	314	1	HEM3_BRUMU
Q6E298	arabidopsis	315	2	Q6E298
Q8FX92	arabidopsis	315	2	Q8FX92
Q8CNA0	staphylococ	315	2	Q8CNA0
Q58654	pyrococcus	316	2	Q58654
Q65VX4	mannheimia	316	2	Q65VX4
Q88121	pseudomonas	316	2	Q88121
Q88121	pseudomonas	316	2	Q88121
Q3PN61	campylobact	317	2	Q3PN61
Q738B9	bacillus ce	317	2	Q738B9
Q738B9	plasmodium	318	2	Q738B9
Q8GTM7	oryza sativ	318	2	Q8GTM7
Q9RHT5	streptomyce	318	2	Q9RHT5
Q82CH1	streptomyce	318	2	Q82CH1
Q89XK4	bradyrhizob	318	2	Q89XK4
Q8KVD3	vibrio chol	318	2	Q8KVD3
Q9PM73	campylobact	318	2	Q9PM73
Q8S6Z9	oryza sativ	319	2	Q8S6Z9
Q83X38	streptomyce	319	2	Q83X38
Q7MT26	porphyromon	319	2	Q7MT26
Q8C187	mus musculu	319	2	Q8C187
Q69996	bacillus su	320	2	Q69996
Q97GF5	clostridium	320	2	Q97GF5
Q73M86	treponema d	320	2	Q73M86
Q67QA9	syndromia d	321	2	Q67QA9
Q986M3	rhizobium l	321	2	Q986M3
Q8310	mus musculu	321	2	Q8310
Q83C4	rhizobium l	322	2	Q83C4
Q8JF6	brachydanio	322	2	Q8JF6
Q6KZU0	picophilius	322	2	Q6KZU0
Q650S2	bacteroides	323	2	Q650S2
Q89XV0	bradyrhizob	323	2	Q89XV0
Q8U0P4	pneumocysti	324	2	Q8U0P4
Q81R12	caecilius an	324	2	Q81R12
Q6HJB5	caecilius th	324	2	Q6HJB5
Q7VZT6	bordetella	325	2	Q7VZT6
Q7W574	bordetella	325	2	Q7W574
Q7WCQ4	bordetella	325	2	Q7WCQ4
Q7Z264	brachydanio	325	2	Q7Z264
Q00030	equine herp	326	1	DUT_EBVA
Q05128	ebola virus	326	1	VP40_EBOZM
Q922R9	rhizobium m	326	2	Q922R9
Q81DZ5	caecilius ce	326	2	Q81DZ5
Q829K7	streptomyce	326	2	Q829K7
Q93251	equid herpe	326	2	Q93251
Q913A4	zaire ebola	326	2	Q913A4
Q77DJ6	zaire ebola	326	2	Q77DJ6
Q9M6R7	psium sativ	327	2	Q9M6R7

689	6	3.9	327	2	QBULJ3	QBul13 agrobacteri	762	6	3.9	346	2	Q9RWH8	Q9rwh8 deinococcus
690	6	3.9	328	1	ABF2_STRCX	P82594 streptomyc	763	6	3.9	347	2	Q8ZSW1	Q8zsw1 pyrobaculum
691	6	3.9	328	1	NCSR_ARATH	P83291 arabidopsis	764	6	3.9	347	2	Q756V5	Q756v5 ashbya goos
692	6	3.9	328	2	Q9D7H2	Q9d7h2 mus musculu	765	6	3.9	347	2	Q8P334	Q8p334 xanthomonas
693	6	3.9	329	2	O18071	O18071 caenorhabdi	766	6	3.9	347	2	Q8XVZ3	Q8xvz3 ralstonia s
694	6	3.9	329	2	Q9MFE7	Q9mfe7 beta vulgar	767	6	3.9	347	2	Q6A6V2	Q6a6v2 propionibac
695	6	3.9	329	2	Q92T16	Q92t16 rhizobium m	768	6	3.9	347	2	Q72M10	Q72m10 leptospira
696	6	3.9	329	2	Q80PX1	Q80px1 human herpe	769	6	3.9	347	2	Q8A2H5	Q8a2h5 bacteroides
697	6	3.9	329	2	Q80PX2	Q80px2 human herpe	770	6	3.9	349	2	O18110	O18110 caenorhabdi
698	6	3.9	329	2	Q80PX3	Q80px3 human herpe	771	6	3.9	349	2	Q86JV0	Q86jv0 dictyosteli
699	6	3.9	329	2	Q80PX4	Q80px4 human herpe	772	6	3.9	350	2	Q56302	Q56302 thermococcu
700	6	3.9	329	2	Q80PX5	Q80px5 human herpe	773	6	3.9	350	2	Q9XUC5	Q9xuc5 caenorhabdi
701	6	3.9	329	2	Q7T1T5	Q7t1t5 bothrops ja	774	6	3.9	350	2	Q8LEX1	Q8lex1 arabidopsis
702	6	3.9	330	2	Q76852	Q76852 tetranychena	775	6	3.9	350	2	Q93283	Q93283 arabidopsis
703	6	3.9	330	2	Q41402	Q41402 sesbania ro	776	6	3.9	350	2	Q928N1	Q928n1 arabidopsis
704	6	3.9	331	1	LDHD_LEUMC	P51011 leuconostoc	777	6	3.9	350	2	Q9ZUB9	Q9zub9 arabidopsis
705	6	3.9	331	2	Q6ZFU6	Q6zfu6 oryza sativ	778	6	3.9	350	2	Q7UPP7	Q7upp7 rhodopirell
706	6	3.9	331	2	Q83359	Q83359 treponema p	779	6	3.9	351	2	O81493	O81493 arabidopsis
707	6	3.9	331	2	Q9JIT7	Q9jit7 cavia porce	780	6	3.9	351	2	Q944K0	Q944k0 arabidopsis
708	6	3.9	331	2	Q8JFX9	Q8jfx9 reston ebol	781	6	3.9	352	1	CYAB_STIAU	P40138 stigmatella
709	6	3.9	332	2	Q96ZS5	Q96z55 sulfolobus	782	6	3.9	352	2	Q6BMG5	Q6bm55 debaryomyce
710	6	3.9	332	2	Q84I39	Q84i39 helicobacte	783	6	3.9	353	2	Q6Z0V7	Q6z0v7 oryza sativ
711	6	3.9	332	2	Q6M925	Q6m925 parachlamyd	784	6	3.9	356	2	Q84I38	Q84i38 helicobacte
712	6	3.9	333	2	O81494	O81494 arabidopsis	785	6	3.9	356	2	Q8NR93	Q8nr93 corynebacte
713	6	3.9	333	2	O87GV7	O87gv7 vibrio para	786	6	3.9	356	2	Q7NVD9	Q7nvd9 chromobacte
714	6	3.9	333	2	Q9JST3	Q9jst3 chlamydia p	787	6	3.9	357	2	P78930	P78930 chlamydia
715	6	3.9	333	2	Q926L1	Q926l1 chlamydia p	788	6	3.9	357	2	Q74FZ0	Q74fz0 geobacter s
716	6	3.9	334	1	PURR_PASMU	Q9cn88 pasteurella	789	6	3.9	357	2	Q9DF34	Q9df34 brachydanio
717	6	3.9	334	2	Q45307	Q45307 caenorhabdi	790	6	3.9	358	2	Q8C2A6	Q8c2a6 mus musculu
718	6	3.9	335	2	Q9UZM6	Q9uzm6 pyrococcus	791	6	3.9	358	2	Q6UDM3	Q6udm3 peitacid h
719	6	3.9	335	2	Q7PWN4	Q7pwn4 anopheles g	792	6	3.9	359	1	AROB_CHRVO	Q7nzu4 chromobacte
720	6	3.9	336	1	XRC4_HUMAN	Q13426 homo sapien	793	6	3.9	359	1	HFE_MOUSE	P70387 mus musculu
721	6	3.9	336	2	Q67MQ8	Q67mq8 symbiobacte	794	6	3.9	359	2	Q6N3V1	Q6n3v1 rhodopseudo
722	6	3.9	336	2	Q84I37	Q84i37 helicobacte	795	6	3.9	359	2	Q8EY15	Q8ey15 leptospira
723	6	3.9	337	2	O58840	O58840 pyrococcus	796	6	3.9	359	2	Q9D754	Q9d754 mus musculu
724	6	3.9	337	2	O8U204	O8u204 pyrococcus	797	6	3.9	361	2	O18068	O18068 caenorhabdi
725	6	3.9	337	2	Q75LX7	Q75lx7 oryza sativ	798	6	3.9	361	2	O8T376	O8t376 meloidogyne
726	6	3.9	337	2	Q84I35	Q84i35 helicobacte	799	6	3.9	362	1	ASG2_YEAST	P11163 saccharomyc
727	6	3.9	337	2	Q73XD2	Q73xd2 mycobacteri	800	6	3.9	362	2	Q6Q5K8	Q6q5k8 saccharomyc
728	6	3.9	337	2	Q89GY5	Q89gy5 bradyrh.zob	801	6	3.9	362	2	Q6Q5K9	Q6q5k9 saccharomyc
729	6	3.9	339	2	Q7MXV9	Q7mxv9 porphyromon	802	6	3.9	362	2	Q7AH88	Q7ah88 escherichia
730	6	3.9	339	2	Q6VZQ0	Q6vzq0 canarypox v	803	6	3.9	362	2	Q6F7E5	Q6f7e5 acinetobact
731	6	3.9	340	2	Q6C875	Q6c875 yarrowia li	804	6	3.9	363	2	Q9NVL6	Q9nvl6 homo sapien
732	6	3.9	340	2	Q69J25	Q69j25 oryza sativ	805	6	3.9	363	2	Q9RKQ5	Q9rkq5 streptomyc
733	6	3.9	340	2	Q8ABQ4	Q8abq4 bacteroides	806	6	3.9	364	2	Q6A6V5	Q6a6v5 propionibac
734	6	3.9	340	2	Q6YCH1	Q6ych1 mus musculu	807	6	3.9	365	1	AROB_PSEPK	Q88cv2 pseudomonas
735	6	3.9	341	2	Q9LMT1	Q9lmt1 arabidopsis	808	6	3.9	365	2	Q8X6B9	Q8x6b9 escherichia
736	6	3.9	341	2	Q6H2J7	Q6h2j7 mycobacteri	809	6	3.9	367	1	AROB_PSESM	Q87v15 pseudomonas
737	6	3.9	341	2	Q6MPL1	Q6mpl1 bdellovibri	810	6	3.9	367	2	O6RCI2	O6rci2 mycobacteri
738	6	3.9	341	2	Q7T5J0	Q7t5j0 cryptophleb	811	6	3.9	367	2	Q7MVZ4	Q7mvz4 porphyromon
739	6	3.9	342	2	Q93KV2	Q93kv2 streptomyc	812	6	3.9	367	2	Q6ZQ44	Q6zq44 mus musculu
740	6	3.9	342	2	Q66IY2	Q66iy2 xenopus lae	813	6	3.9	368	1	AROB_PSEAE	P34002 pseudomonas
741	6	3.9	342	2	Q6DFQ7	Q6dfq7 xenopus tro	814	6	3.9	369	1	HI82_PSEAE	Q9h268 pseudomonas
742	6	3.9	343	2	O84I34	O84i34 helicobacte	815	6	3.9	369	2	Q979M3	Q979m3 thermoplas
743	6	3.9	343	2	O8Y414	O8y414 listeria mo	816	6	3.9	369	2	Q9HJK0	Q9hjk0 thermoplas
744	6	3.9	343	2	Q92TH6	Q92th6 listeria in	817	6	3.9	369	2	Q84I36	Q84i36 helicobacte
745	6	3.9	343	2	Q71WA8	Q71wa8 listeria mo	818	6	3.9	369	2	Q6NIM2	Q6nim2 corynebacte
746	6	3.9	344	1	PILT_PSEAE	P24559 pseudomonas	819	6	3.9	370	1	HUPK_RHLIV	P28153 rhizobium l
747	6	3.9	344	2	Q7BTG5	Q7btg5 pseudomonas	820	6	3.9	370	2	Q6BRJ2	Q6brj2 debaryomyce
748	6	3.9	344	2	Q9F667	Q9f667 pseudomonas	821	6	3.9	370	2	Q7QQ57	Q7qq57 giardia lam
749	6	3.9	344	2	Q87CD4	Q87cd4 xylella fas	822	6	3.9	370	2	Q916T2	Q9i6t2 pseudomonas
750	6	3.9	344	2	Q87V94	Q87v94 pseudomonas	823	6	3.9	371	2	Q93NC0	Q93nc0 myxococcus
751	6	3.9	344	2	Q9PCX1	Q9pcx1 xylella fas	824	6	3.9	371	2	Q67JF5	Q67jf5 symbiobacte
752	6	3.9	345	1	ADD_RALSO	O8xx15 ralstonia s	825	6	3.9	372	1	DNAJ_BACSU	P17631 bacillus su
753	6	3.9	345	1	CYSA_VIBVU	Q8d653 vibrio vuln	826	6	3.9	372	2	Q8YU49	Q8yua9 anabaena sp
754	6	3.9	345	1	VAOD_YEAST	P32366 saccharomyc	827	6	3.9	373	2	Q8P402	Q8p402 xanthomonas
755	6	3.9	345	2	Q8NL23	Q8nl23 xanthomonas	828	6	3.9	374	2	Q9PTL7	Q9ptl7 xenopus lae
756	6	3.9	345	2	Q7CLR1	Q7clr1 xanthomonas	829	6	3.9	376	1	Y5D9_GLOVI	Q7ndu3 gloebacter
757	6	3.9	345	2	Q7PIN4	Q7pin4 chromobacte	830	6	3.9	376	2	Q9Y8P6	Q9y8p6 aeropyrum p
758	6	3.9	346	1	LUXA_PHOFO	P24113 photobacter	831	6	3.9	376	2	Q7PQV5	Q7pqv5 anopheles g
759	6	3.9	346	2	Q97ZH7	Q97zh7 sulfolobus	832	6	3.9	376	2	Q67L31	Q67l31 symbiobacte
760	6	3.9	346	2	Q7WP94	Q7wp94 bordetella	833	6	3.9	376	2	Q6D5Y0	Q6d5y0 erwinia car
761	6	3.9	346	2	Q89LP2	Q89lp2 bradyrhizob	834	6	3.9	376	2	O37387	O37387 common chim

835	376	2	Q801S9	Q801S9 xenopus lae	908
836	377	1	Q8GHY5	Q8ghy5 pseudomonas	909
837	378	1	FLIY_BACSU	P24073 bacillus su	910
838	378	2	Q7X2A0	Q7x2a0 pseudomonas	911
839	380	2	Q6CHZ1	Q6chz1 yarrowia li	912
840	380	2	Q73R97	Q73r97 treponema d	913
841	380	2	Q9K000	Q9k000 neisseria m	914
842	381	1	ARGE_BUCAI	P57155 buchnera ap	915
843	381	2	Q8BIM3	Q8bim3 mus musculus	916
844	384	2	Q6VZP9	Q6vzp9 oryza sativ	917
845	384	2	Q8EX13	Q8ex13 streptomyce	918
846	386	1	ARGJ_CORDI	P62059 corynebacte	919
847	386	1	CUE1_HUMAN	Q9nmw3 homo sapien	920
848	386	2	Q7PK57	Q7pk57 anopheles g	921
849	386	2	Q64094	Q64094 bacterioph	922
850	386	2	Q31927	Q31927 bacillus su	923
851	386	2	Q8BJJ5	Q8bjj5 rhizobium l	924
852	386	2	Q8FEJ4	Q8fej4 acinetobact	925
853	388	1	CUE1_MOUSE	Q8r3v6 mus musculu	926
854	388	2	Q8ZYI9	Q8zyi9 pyrobaculum	927
855	388	2	Q96Z16	Q96z16 sulfolobus	928
856	388	2	Q16881	Q16881 caenorhabdi	929
857	388	2	Q8KE01	Q8ke01 chlorobium	930
858	389	2	Q6LYW7	Q6lyw7 methanococc	931
859	389	2	Q6N4F5	Q6n4f5 rhodopsedo	932
860	389	2	Q89IU8	Q89iu8 bradyrhizob	933
861	389	2	Q8DJV0	Q8djv0 synechococ	934
862	390	2	Q22101	Q22101 caenorhabdi	935
863	391	1	PCL_ECTHA	P42516 ectothiorho	936
864	391	2	Q7JNC6	Q7jnc6 desophilia	937
865	391	2	Q7QG4Y	Q7qgy4 anopheles g	938
866	391	2	Q02690	Q02690 podospora a	939
867	391	2	Q8D5A1	Q8d5a1 vibrio vuln	940
868	392	1	LVC1_YARLI	P41929 yarrowia li	941
869	392	2	Q8Z9Y0	Q8z9y0 oryza sativ	942
870	392	2	Q8GALO	Q8gal0 athrobacte	943
871	392	2	Q8GLG9	Q8glg9 streptomyce	944
872	393	2	Q7Y0Z8	Q7y0z8 lycopersico	945
873	393	2	Q8RR83	Q8rr83 acetobacter	946
874	393	2	Q821D8	Q821d8 mus musculu	947
875	394	2	Q8M220	Q8m220 methylocyst	948
876	394	2	Q8RENE	Q8ren6 fusobacteri	949
877	394	2	Q6A5K4	Q6a5k4 propionibac	950
878	394	2	Q7VVV1	Q7vvv1 bordetella	951
879	394	2	Q7WKJ9	Q7wkj9 bordetella	952
880	394	2	Q8KB99	Q8kb99 bacillus ha	953
881	395	2	Q7XEG1	Q7xeg1 oryza sativ	954
882	395	2	Q6EVS8	Q6evs8 yersinia ps	955
883	395	2	Q9KZC2	Q9kzc2 streptomyce	956
884	396	2	Q6BJ17	Q6bj17 debaryomyce	957
885	396	2	Q8UAU3	Q8uau3 caenorhabdi	958
886	398	2	Q878Z4	Q878z4 thermoplas	959
887	398	2	Q85765	Q85765 saccharomyc	960
888	398	2	Q63R97	Q63r97 burkholderi	961
889	399	2	Q8HGNE	Q8hgn6 schizosacch	962
890	399	2	Q8L912	Q8l912 arabidopsis	963
891	399	2	Q8M9V4	Q8m9v4 arabidopsis	964
892	399	2	Q8BZF1	Q8bzfi mus musculu	965
893	400	2	Q9GZH7	Q9gzh7 caenorhabdi	966
894	400	2	Q8N8Z6	Q8n8z6 rhodopsedo	967
895	400	2	Q73ND4	Q73nd4 treponema d	968
896	400	2	Q6P6Q1	Q6p6q1 mus musculu	969
897	401	2	Q8P6E3	Q8p6e3 rhizobium l	970
898	401	2	Q7U8J2	Q7u8j2 synechococc	971
899	402	2	Q8KE54	Q8ke54 chlorobium	972
900	402	2	Q7V4M1	Q7v4m1 prochloroco	973
901	402	2	Q6D669	Q6d669 erwinia car	974
902	402	2	Q9W5Z9	Q9w5z9 fugu rubrip	975
903	403	2	Q742P6	Q742p6 mycobacteri	976
904	404	2	Q7QY67	Q7qy67 giardia lam	977
905	404	2	Q7MC72	Q7mc72 vibrio vuln	978
906	405	2	Q97ZT8	Q97zt8 sulfolobus	979
907	405	2	Q9AXJ7	Q9axj7 medicago tr	980

Q8rn03	amycolatops	980
Q941e5	cyanidiosch	909
Q6cqm8	kluyveromyc	910
Q6ncv1	rhodopsedo	911
Q7ps28	anopheles g	912
Q65zt1	borrelia ga	913
Q6jkt4	zootermopsi	914
Q6jkt7	zootermopsi	915
Q9ahf3	lysobacter	916
Q9yct5	aeropyrum p	917
Q9pt10	anopheles g	918
Q7w783	bordetella	919
Q8n6e0	homo sapien	920
Q9hej0	neuropora	921
Q9nal6	caenorhabdi	922
Q6lpk3	photobacter	923
Q7v099	prochloroco	924
Q8lp50	lunaria ann	925
Q6sgb2	uncultured	926
Q7w0p6	bordetella	927
Q7w3f8	bordetella	928
Q7wes8	bordetella	929
Q63h22	bacillus ce	930
Q81iy9	bacillus ce	931
Q81vl5	bacillus an	932
Q8dsq3	streptococc	933
Q9en19	homo sapien	934
Q6rc07	mycobacteri	935
Q64nz1	bacteroides	936
Q91gf4	epiphyas po	937
Q90za4	ambystoma m	938
Q84di2	caulobacter	939
Q84di5	caulobacter	940
Q84di8	caulobacter	941
Q84dj5	caulobacter	942
Q73f05	bacillus ce	943
Q8fq66	corynebacte	944
Q6hpj5	bacillus th	945
Q9vzw8	desophilia	946
Q9pvs6	methanosarc	947
Q6x8l3	homo sapien	948
Q86un3	homo sapien	949
Q7we84	bordetella	950
Q83a86	coxiella bu	951
Q8aet0	leifsonia x	952
Q9ax61	arabidopsis	953
Q82017	nitrosomona	954
Q70in2	pseudomonas	955
Q63bu5	bacillus ce	956
Q6f735	acinetobact	957
Q7ul99	rhodopirell	958
Q76652	caenorhabdi	959
Q6jt24	ornithocoon	960
Q8nab8	homo sapien	961
Q76iq2	candida gla	962
Q8as48	encephalito	963
Q97ah4	thermoplas	964
Q7m161	vibrio vuln	965
Q80770	emericella	966
Q87ly3	vibrio para	967
Q8dbx8	vibrio vuln	968
Q7mtj6	porphyromon	969
Q7cu40	prochloroco	970
Q9ku97	vibrio chol	971
Q94c40	arabidopsis	972
Q9x804	streptomyce	973
P42258	haloarcula	974
Q8ynq2	anabena sp	975
Q7v019	prochloroco	976
Q9a386	caulobacter	977
Q07364	chlamydia t	978
O84099	chlamydia t	979


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Qy 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 120
Db 328 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 387

Qy 121 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 153
Db 388 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 420

RESULT 3
Q8WYF7 PRELIMINARY; PRT; 964 AA.
AC Q8WYF7;
DT 01-MAR-2002 (TReMBLrel. 20, Created)
DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE POB1.
GN Name=POB1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMEL; AB020705; BAA74921.1; -.
DR Genew; HGNC:7523; TRIM37.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf-like.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
FT NON TER 1
SQ SEQUENCE 979 AA; 109607 MW; D9958FE2EA23EEFD CRC64;

Query Match 100.0%; Score 153; DB 2; Length 964;
Best Local Similarity 100.0%; Pred. No. 3.6e-155;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 60
Db 268 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 327

Qy 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 120
Db 328 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 387

Qy 121 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 153
Db 388 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 420

RESULT 4
ID Q94972 PRELIMINARY; PRT; 979 AA.
AC Q94972;
DT 01-MAY-1999 (TReMBLrel. 10, Created)
DT 01-MAY-1999 (TReMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE KIAA0898 protein (Fragment).
GN Name=KIAA0898;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMEL; AB020705; BAA74921.1; -.
DR Genew; HGNC:7523; TRIM37.
DR GO; GO:000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf-like.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
FT NON TER 1
SQ SEQUENCE 979 AA; 109607 MW; D9958FE2EA23EEFD CRC64;

Query Match 100.0%; Score 153; DB 2; Length 979;
Best Local Similarity 100.0%; Pred. No. 3.7e-155;
Matches 153; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 60
Db 283 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGNVGRGYLSV 342

Qy 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 120
Db 343 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFVGCWGNRRFRLLDLANE 402

Qy 121 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 153
Db 403 GYLNPQNDTVILRFQVRSPTFFQKSRDQHWYIT 435

RESULT 5
Q8CHC5 PRELIMINARY; PRT; 928 AA.
AC Q8CHC5;
DT 01-MAR-2003 (TReMBLrel. 23, Created)
DT 01-MAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE KIAA0898 protein (Fragment).
GN Name=KIAA0898;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB093271; BAC41455.1; -.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
```

```
DR InterPro: IPR003649; Bbox_C.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR008974; Traf_Like.
DR InterPro: IPR000315; Znf_Box.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00643; zf-B_box; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00502; BBC; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00061; MATH; 1.
DR PROSITE: PS01144; MATH; 1.
DR PROSITE: PS0119; ZF_BOX; 1.
DR NON_TER 1
SQ SEQUENCE 928 AA; 103732 MW; 23CEODAAD85BFDE CRC64;

Query Match 81.0%; Score 124; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 5.4e-124;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGVGYLSV 60
Db 235 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGVGYLSV 294

QY 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWYGNRFRRLDLLANE 120
Db 295 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWYGNRFRRLDLLANE 354

QY 121 GYLN 124
Db 355 GYLN 358

RESULT 6
Q6PCX9 PRELIMINARY; PRT; 961 AA.
AC Q6PCX9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tripartite motif protein 37.
GN Name=Trim37;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22389257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzyzanski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.
PT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
```

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RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059070; AAH59070.1; -.
DR EMBL; BC058678; AAH58678.1; -.
DR GO; GO:0016015; F:morphogen activity; TAS.
DR GO; GO:0003649; Bbox_C.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR008974; Traf_Like.
DR InterPro: IPR000315; Znf_Box.
DR InterPro: IPR001841; Znf_Ring.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS01144; MATH; 1.
DR PROSITE; PS0119; ZF_BOX; 1.
DR PROSITE; PS0089; ZF_RING_2; 1.
SQ SEQUENCE 961 AA; 107659 MW; 85629CBFE0A1D6EA CRC64;

Query Match 81.0%; Score 124; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 5.5e-124;
Matches 124; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGVGYLSV 60
Db 268 FTSELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDNGVGVGYLSV 327

QY 61 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWYGNRFRRLDLLANE 120
Db 328 FLELSAGLPETSKYEYRVMVHQSCNDPTKNIREFASDFEVCWYGNRFRRLDLLANE 387

QY 121 GYLN 124
Db 388 GYLN 391

RESULT 7
Q95LW3 PRELIMINARY; PRT; 721 AA.
AC Q95LW3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Oada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
RL in the human genome sequence."
RL BMC Genomics 3:36-36(2002).
DR EMBL; AB071078; BAB64471.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR008974; Traf_Like.
DR InterPro: IPR001841; Znf_Ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00089; ZF_RING_2; 1.
KW Hypothetical protein_RING_2; 1.
SQ SEQUENCE 721 AA; 80131 MW; 203B974760F866E9 CRC64;
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Query Match 51.6%; Score 79; DB 2; Length 721;
 Best Local Similarity 100.0%; Pred. No. 1e-75;
 Matches 79; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 75 EYRVMHQSCNDPTKNIIRFASDFEVEGCGWYNNRFRLLDANEGYLNPNQDVTILRF 134
 Db 100 EYRVMHQSCNDPTKNIIRFASDFEVEGCGWYNNRFRLLDANEGYLNPNQDVTILRF 159

Qy 135 QVRSPTFFQKSRDQHWYIT 153
 Db 160 QVRSPTFFQKSRDQHWYIT 178

RESULT 8
 ID G101 HUMAN STANDARD; PRT; 508 AA.
 AC Q96P66; QNG93;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Probable G protein-coupled receptor GPR101.
 GN Name=GPR101;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
 RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
 RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
 RT "Discovery and mapping of ten novel G protein-coupled receptor
 genes";
 RL Gene 275:83-91 (2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040266; PubMed=144878; DOI=10.1016/S0014-5793(02)02775-8;
 RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
 RT "Identification of G protein-coupled receptor genes from the human
 genome sequence";
 RL FEBS Lett. 520:97-101 (2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX Suwa M., Sato T., Okouchi I., Arita M., Futami K., Matsumoto S.,
 RA Teutsumi S., Aburatani H., Asai K., Akiyama Y.;
 RT "Genome-wide discovery and analysis of human seven transmembrane helix
 receptor genes";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Orphan receptor.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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EMBL; AF411115; AAL26486.1; --
 DR EMBL; AB083588; BAB9301.1; --
 DR EMBL; AB065937; BAC0612.1; ALT_INIT.
 DR Genbank; HGNC:14963; GPR101.
 DR MIM; 300393; --
 DR InterPro; IPR000276; GPCR_Rhodpsn.
 DR Pfam; PF00001; 7tm.1.1;
 DR PRINTS; PF00237; GPCR_Rhodopsin
 DR PROSITE; PS00237; G_PROTEIN_RCEP_F1_1; 1.
 DR PROSITE; PS00262; G_PROTEIN_RCEP_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.
 DOMAIN 1 35 Extracellular (Potential).

TRANSMEM 36 56 1 (Potential).
 DOMAIN 57 68 Cytoplasmic (Potential).
 FT 69 89 2 (Potential).
 FT 90 106 Extracellular (Potential).
 FT 107 127 3 (Potential).
 FT 128 149 Cytoplasmic (Potential).
 FT 150 170 4 (Potential).
 FT 171 196 Extracellular (Potential).
 FT 197 217 5 (Potential).
 FT 218 399 Cytoplasmic (Potential).
 FT 400 420 6 (Potential).
 FT 421 433 Extracellular (Potential).
 FT 434 454 7 (Potential).
 FT 455 508 Cytoplasmic (Potential).
 FT DISULFID 104 182 By similarity.
 FT CARBOHYD 7 7 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 13 13 N-linked (GlcNAc...) (Potential).
 SQ SEQUENCE 508 AA; 56716 MW; E20A409F5C95B85 CRC64;

Query Match 5.9%; Score 9; DB 1; Length 508;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 VPSYDSATP 14
 Db 499 VPSYDSATP 507

RESULT 9
 O34947 PRELIMINARY; PRT; 210 AA.
 AC O34947; O796E9;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Yoaz.
 GN Name=Yoaz; OrderedLocusNames=BSU18790;
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
 RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
 RA Borriass R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Gim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M.,
 RA Jones L.-M., Joris B., Karamata D., Kasehara Y., Klacerr-Blanchard M.,
 RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
 RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
 RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maugel C.,
 RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
 RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudga B.,
 RA Park S.H., Parro V., Pohl T.M., Portetelle D., Porwollik S.,
 RA Prescott A.M., Presecan E., Pujic P., Purnelle B., Rapoport G.,
 RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
 RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroeter R.,
 RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serro P.,
 RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
 RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpetra P.,
 RA Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vannier F.,

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RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
DR EMBL; AF027868; AAB84456.1; -.
DR EMBL; Z99114; CAB13771.1; -.
DR FIR; A69898; A69898.
DR InterPro; IPR002818; ThiJ/Pfpi.
DR Pfam; PF01965; DJ_1_pfp1; 1.
KW Complete proteome.
SQ SEQUENCE 210 AA; 23420 MW; 18A8BA915AAEF745 CRC64;

Query Match 5.2%; Score 8; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 117 LANEGYLN 124
Db 116 LANEGYLN 123

RESULT 10
Q65003 PRELIMINARY; PRT; 286 AA.
AC Q65003;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative cell-to-cell movement protein.
OS Apple mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OC NCBI_TaxID=12319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95374352; PubMed=7646355;
RA Shiel P.J., Alfesai R.H., Domier L.L., Korban S.S., Berger P.H.;
RT "The complete nucleotide sequence of apple mosaic virus RNA-3.";
RL Arch. Virol. 140:1247-1256(1995).
DR EMBL; U15608; AAB86960.1; -.
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP; 1.
SQ SEQUENCE 286 AA; 32409 MW; D2A4493315AB82C1 CRC64;

Query Match 5.2%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 98 SDFEVGEC 105
Db 10 SDFEVGEC 17

RESULT 11
Q63CU1 PRELIMINARY; PRT; 423 AA.
AC Q63CU1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase/deaminase family protein.
GN ORFNames=BTZK1681;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ZK;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
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RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CP000001; AAU18572.1; -.
KW Hydrolase.
SQ SEQUENCE 423 AA; 46816 MW; BD583BC7F209A87B CRC64;

Query Match 5.2%; Score 8; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 EFASDFEV 102
Db 27 EFASDFEV 34

RESULT 12
Q81S14 PRELIMINARY; PRT; 435 AA.
AC Q81S14; Q61094; Q6K068;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase family protein.
GN OrderedLocustNames=BA1865, BA1729, GBAA1865;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
RX MEDLINE=22608414; PubMed=12721629; DOI=10.1038/nature01586;
RA Read T.D., Peterson S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapfel E.K., Ostad O.A., Helgason E., Rillstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahmoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Platt R.D., Wolf A.M., Watkins K.L., Niernan W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaitte J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koehler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.F., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=Sterne;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017030; AAP25768.1; -.
DR EMBL; AE017334; AAT30980.2; -.
DR EMBL; AE017225; AAT54045.1; -.
DR HSP; O9X034; 1p1M.
DR TIGR; BA1865; -.
DR TIGR; GBAA1865; -.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro 1.
DR InterPro; IPR011550; Amidohydro like.
DR InterPro; IPR011059; Metallo_hydrolase.
DR Pfam; PF01979; Amidohydro 1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.
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KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48143 MW; 2D9289BAA5819B33 CRC64;

Query Match 5.2%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred.No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 EFASDFEV 102
Db 39 EFASDFEV 46

RESULT 13
Q6HK87 PRELIMINARY; PRT; 435 AA.
AC Q6HK87;
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chlorohydrolase/deaminase family protein.
GN OrderedLocusNames=BT9727.1707;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Brettin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Kelm P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27."
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL: AE017355; AAT59611.1; -
DR GO: GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro_like.
DR Pfam; PF01979; Metallo_hydrolase.
DR ProDom; PD01248; Amidohydro_1; 1.
DR Complete proteome; Hydrolase.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48139 MW; 68EE505358A83268 CRC64;

Query Match 5.2%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred.No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 EFASDFEV 102
Db 39 EFASDFEV 46

RESULT 14
Q8E8R3 PRELIMINARY; PRT; 1045 AA.
AC Q8E8R3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heavy metal efflux pump, CzcA family.
GN OrderedLocusNames=SO4598;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbc749;
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Teapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Unayam L.A.,

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RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis."
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL: AE015891; AAN57558.1; -.
DR TIGR; SO4598; -.
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0008324; F:cation transporter activity; IEA.
DR GO: GO:0006812; P:cation transport; IEA.
DR InterPro; IPR003439; ABC transporter.
DR InterPro; IPR001036; Acrflavin_res.
DR InterPro; IPR004763; CzcA.
DR Pfam; PF00873; Acr_tran; 1.
DR PRINTS; PRO0702; ACRIFLAVINRP.
DR TIGRFAMs; TIGR00914; ZAO601; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1045 AA; 114513 MW; 9E99187C3248C984 CRC64;

Query Match 5.2%; Score 8; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred.No. 32;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 63 ELSAGLPE 70
Db 311 ELSAGLPE 318

RESULT 15
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AC Q89T67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bel2183 protein.
GN OrderedLocusNames=bsl2183;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idegawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimpō S., Teiruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005942; BAC47448.1; -.
KW Complete proteome.
SQ SEQUENCE 98 AA; 10886 MW; 90279D1E01E99AD5 CRC64;

Query Match 4.6%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred.No. 45;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 127 NDTVILR 133
Db 39 NDTVILR 45

Search completed: July 20, 2005, 20:51:41
Job time : 143.45 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:37:15 ; Search time 87.75 Seconds
(without alignments)
787.814 Million cell updates/sec

Title: US-09-706-325-25

Perfect score: 135

Sequence: 1 ELVPSYDSATFLENFSTLR.....NEGYLNPNQDVTILRFQVRS 135

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	135	100.0	964	2	Q81YF7
3	135	100.0	964	2	Q8WYF7
4	135	100.0	979	2	Q94972
5	121	89.6	928	2	Q8CHCS
6	121	89.6	961	2	Q6PCX9
7	64	47.4	721	2	Q95LW3
8	9	6.7	508	1	G101_HUMAN
9	8	5.9	210	2	Q34947
10	8	5.9	286	2	Q85003
11	8	5.9	423	2	Q63CU1
12	8	5.9	435	2	Q81S14
13	8	5.9	435	2	Q6HK87
14	8	5.9	1045	2	Q8E8R3
15	7	5.2	98	2	Q89T67
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17	7	5.2	174	2	Q7P7W8
18	7	5.2	198	2	Q46025
19	7	5.2	198	2	Q6NGT3
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21	7	5.2	246	2	Q82FC0
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23	7	5.2	255	2	Q74D44
24	7	5.2	257	2	Q9WXV4
25	7	5.2	261	2	Q70EC9
26	7	5.2	278	2	Q7UEF2
27	7	5.2	285	2	Q9UZA2
28	7	5.2	307	2	Q87TD8
29	7	5.2	316	2	Q9XWH8
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Q8yfw9	brucella me
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Q6iuv3	halobacillu
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Q81sc6	bacillus ce
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Q8et62	oceanobacil
Q6hb48	bacillus th
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Q7nq38	chromobacte
P5417	bacillus su
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Q7mv63	porphyromon
Q7r282	giardia lam
Q9xil9	arabidopsis
Q6z0u0	oryza sativ
Q8541	hordeum vul
Q8fyf0	hordeum vul
Q91k09	plasmodium
Q8s7s8	hordeum vul
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245	6	4.4	147	2	Q737P5	Q737p5 bacillus ce
246	6	4.4	148	2	Q22500	Q22500 caenorhabdi
247	6	4.4	149	1	Y281_LEIXX	Q6ah32 leifsonia x
248	6	4.4	149	2	Q890I2	Q890i2 lactobacill
249	6	4.4	150	2	Q66086	Q66086 canine hearp
250	6	4.4	153	2	Q64A10	Q64a10 uncultured

251	6	4.4	153	2	Q8YJQ9	Q8YJQ9 brucella me	324	6	4.4	191	1	PTH_MYCBO	P55866 mycobacteri
252	6	4.4	154	2	Q7M1Z7	Q7m1z7 daucus caro	325	6	4.4	191	1	PTH_MYCTU	P55865 mycobacteri
253	6	4.4	154	2	Q7XZ67	Q7xz67 griffithsia	326	6	4.4	191	2	Q741V9	Q741v9 mycobacteri
254	6	4.4	155	2	Q7VP20	Q7vp20 haemophilus	327	6	4.4	193	1	YN42_CAUCR	Q9a5v5 caulobacter
255	6	4.4	157	2	Q8DXN3	Q8dxn3 streptococc	328	6	4.4	193	2	Q9NX89	Q9nx89 homo sapien
256	6	4.4	158	2	Q8XQL8	Q8xql8 ralsstonia s	329	6	4.4	194	2	Q66080	Q66080 canine harp
257	6	4.4	158	2	Q7VL01	Q7vl01 haemophilus	330	6	4.4	196	2	Q6FDU6	Q6fdue acinetobact
258	6	4.4	159	2	P73640	P73640 synechocyst	331	6	4.4	196	2	Q83DI8	Q83dl8 coxiella bu
259	6	4.4	160	2	Q7N1H1	Q7nh1 photorhabdu	332	6	4.4	197	2	Q9VZ32	Q9vz32 drosophila
260	6	4.4	161	1	RL11_METWA	Q8py53 methanosarc	333	6	4.4	198	2	Q7RV81	Q7rvr1 neurospora
261	6	4.4	161	2	Q8U4L4	Q8u4l4 pyrococcus	334	6	4.4	198	2	Q6VY95	Q6vy95 oryza sativ
262	6	4.4	161	2	Q9HB69	Q9hb69 homo sapien	335	6	4.4	199	1	PTH_MYCLE	Q8cd49 mycobacteri
263	6	4.4	161	2	Q32085	Q32085 bacillus su	336	6	4.4	199	2	Q8PA66	Q8pa66 xanthomonas
264	6	4.4	161	2	Q7ME07	Q7me07 vibrio vuln	337	6	4.4	200	2	Q9WX32	Q9px32 human herpe
265	6	4.4	161	2	Q7WE75	Q7we75 bordetella	338	6	4.4	200	2	Q9W8K2	Q9wk82 human herpe
266	6	4.4	161	2	Q6S9W2	Q6s9w2 columbid ci	339	6	4.4	200	2	Q9YUA9	Q9yu9 human immun
267	6	4.4	162	2	Q64EG2	Q64eg2 uncultured	340	6	4.4	201	2	Q7QNV9	Q7qnv9 giardia lam
268	6	4.4	162	2	Q87Z67	Q87z67 pseudomonas	341	6	4.4	201	2	Q7YXH2	Q7yxh2 caenorhabdi
269	6	4.4	164	2	Q05127	Q05127 neisseria g	342	6	4.4	202	2	Q6V0K5	Q6v0k5 mycobacteri
270	6	4.4	165	2	Q98LE9	Q98le9 rhizobium l	343	6	4.4	203	2	Q9KMZ7	Q9kmz7 vibrio chol
271	6	4.4	165	2	Q747H7	Q747h7 geobacter s	344	6	4.4	204	2	Q9RC46	Q9rc46 bacillus ha
272	6	4.4	166	2	Q6XND3	Q6xnd3 rhodococcus	345	6	4.4	204	2	Q98HN0	Q98hn0 rhizobium l
273	6	4.4	171	1	YCBV_ECOLI	P75860 escherichia	346	6	4.4	205	2	Q8ID59	Q8id59 plasmodium
274	6	4.4	171	2	Q8PHF9	Q8phf9 xanthomonas	347	6	4.4	205	2	Q9HZD9	Q9hzd9 pseudomonas
275	6	4.4	171	2	Q82N41	Q82n41 streptomyce	348	6	4.4	206	1	YX59_PSESM	Q87zr5 pseudomonas
276	6	4.4	172	2	Q87CK2	Q87ck2 xylella fas	349	6	4.4	206	2	Q74N80	Q74n80 nanoarchaeu
277	6	4.4	172	2	Q912Q0	Q912q0 pseudomonas	350	6	4.4	206	2	Q7PIX6	Q7pix6 anopheles g
278	6	4.4	175	2	Q84R71	Q84r71 oryza sativ	351	6	4.4	206	2	Q86EJ3	Q86ej3 schistosoma
279	6	4.4	177	2	Q81RP2	Q81rp2 drosophila	352	6	4.4	206	2	Q8BRQ1	Q8brq1 mus musculus
280	6	4.4	178	2	Q8ZY10	Q8zy10 pyrobaculum	353	6	4.4	208	1	Y4B5_PSEPK	Q88fr8 pseudomonas
281	6	4.4	178	2	Q87051	Q87051 pseudocardi	354	6	4.4	208	2	Q8H014	Q8h014 oryza sativ
282	6	4.4	178	2	Q87568	Q87568 helicobacte	355	6	4.4	208	2	Q8YHJ5	Q8yhj5 bruceella me
283	6	4.4	178	2	Q8CR93	Q8cr93 staphylococ	356	6	4.4	209	1	GEMI_HUMAN	Q75496 homo sapien
284	6	4.4	178	2	Q8A5S1	Q8a5s1 caulobacter	357	6	4.4	211	2	Q8BSI3	Q8bsl3 mus musculus
285	6	4.4	179	2	Q7QINO	Q7qino anopheles g	358	6	4.4	212	2	Q9C9K9	Q9c9k9 arabisopsis
286	6	4.4	179	2	Q87VNO	Q87vno pseudomonas	359	6	4.4	212	2	Q85372	Q85372 rhodococcus
287	6	4.4	179	2	Q88HE4	Q88he4 pseudomonas	360	6	4.4	213	2	Q65EF8	Q65ef8 bacillus li
288	6	4.4	179	2	Q9QUC6	Q9quc6 tt virus. o	361	6	4.4	213	2	Q7UWS1	Q7uws1 rhodopirell
289	6	4.4	180	2	Q8Q971	Q8q971 neisseria g	362	6	4.4	214	2	Q7Q2M4	Q7q2m4 anopheles g
290	6	4.4	180	2	Q8G0B3	Q8g0b3 brucella su	363	6	4.4	214	2	Q657Y6	Q657y6 oryza sativ
291	6	4.4	181	2	Q74KA6	Q74ka6 lactobacill	364	6	4.4	215	1	RFB5_CANGA	Q65qa6 candida gla
292	6	4.4	181	2	Q7DD77	Q7dd77 neisseria m	365	6	4.4	215	1	RFB5_YEAST	P20434 saccharomyc
293	6	4.4	181	2	Q9JQN6	Q9jqn6 neisseria m	366	6	4.4	215	2	Q9XEX0	Q9xex0 gracilaria
294	6	4.4	182	2	Q04410	Q04410 raphanus sa	367	6	4.4	215	2	Q8X4E4	Q8x4e4 escherichia
295	6	4.4	182	2	Q8RVZ1	Q8rvz1 bifidobacte	368	6	4.4	217	2	Q72A59	Q72a59 desulfovibr
296	6	4.4	182	2	Q8DJX9	Q8djx9 synechococc	369	6	4.4	218	1	YD12_MYCPN	P75469 mycoplasma
297	6	4.4	183	1	DIN1_RAPSA	P27626 raphanus sa	370	6	4.4	218	2	Q754S6	Q754s6 ashbya gos8
298	6	4.4	183	2	Q21131	Q21131 caenorhabdi	371	6	4.4	219	2	Q9AS64	Q9as64 oryza sativ
299	6	4.4	183	2	Q9HXU2	Q9hxu2 pseudomonas	372	6	4.4	222	2	Q7WGT6	Q7wgt6 bordetella
300	6	4.4	184	2	Q8JF87	Q8jf87 human immun	373	6	4.4	223	2	Q972K5	Q972k5 sulfolobus
301	6	4.4	185	2	Q8A357	Q8a357 bacteroides	374	6	4.4	223	2	Q7VT24	Q7vtz4 bordetella
302	6	4.4	186	1	RRF_RHOBA	Q7uch0 rhodopirell	375	6	4.4	223	2	Q7WK92	Q7wk92 bordetella
303	6	4.4	186	1	TNR5_PSEAE	P06691 pseudomonas	376	6	4.4	224	2	Q82M30	Q82m30 streptomyc
304	6	4.4	186	1	TNR7_ECOLI	P06692 escherichia	377	6	4.4	224	2	Q9RU88	Q9ru88 deinococcus
305	6	4.4	186	2	Q66046	Q66046 pseudomonas	378	6	4.4	225	2	Q92BV3	Q92bv3 streptomyc
306	6	4.4	186	2	Q934S3	Q934s3 thiobacillu	379	6	4.4	226	2	Q33188	Q33188 mycobacteri
307	6	4.4	186	2	Q8EB60	Q8eb60 aeromonas p	380	6	4.4	226	2	Q7TZS6	Q7tzes6 mycobacteri
308	6	4.4	186	2	Q7AXT9	Q7axt9 pseudomonas	381	6	4.4	227	2	Q6C587	Q6c587 yarrowia li
309	6	4.4	186	2	Q7BEI7	Q7bei7 shigella fl	382	6	4.4	227	2	Q7MUR2	Q7mur2 porphyromon
310	6	4.4	186	2	Q9AJD0	Q9ajd0 pseudomonas	383	6	4.4	227	2	Q9RWX2	Q9rwx2 deinococcus
311	6	4.4	186	2	Q65IT1	Q65it1 bacillus li	384	6	4.4	230	1	AQPZ_PSEPK	Q88f17 pseudomonas
312	6	4.4	187	2	Q7AG38	Q7ag38 escherichia	385	6	4.4	230	1	UL16_HCMVA	P16757 human cytom
313	6	4.4	187	2	Q8X581	Q8x581 escherichia	386	6	4.4	230	2	Q7MF85	Q7mf85 human cytom
314	6	4.4	187	2	Q83RX8	Q83rx8 shigella fl	387	6	4.4	230	2	Q7TF85	Q7tf85 symbiobacte
315	6	4.4	188	2	Q30134	Q30134 archaeoglob	388	6	4.4	231	2	Q67SV4	Q67sv4 desulfitoba
316	6	4.4	188	2	P73277	P73277 synechocyst	389	6	4.4	232	2	Q9LAS2	Q9las2 salmoneila
317	6	4.4	188	2	Q9JL38	Q9jl38 mus musculu	390	6	4.4	232	2	Q8ZN09	Q8zn09 lactobacill
318	6	4.4	189	2	Q74323	Q74323 s signal pe	391	6	4.4	232	2	Q741I1	Q741i1 pneumocysti
319	6	4.4	189	2	Q8A356	Q8a356 bacteroides	392	6	4.4	233	2	P78728	P78728 pneumocysti
320	6	4.4	189	2	Q9FCH8	Q9pch8 xylella fas	393	6	4.4	233	2	P78730	P78730 mycobacteri
321	6	4.4	190	1	CYGB_HUMAN	Q8wmm9 homo sapien	394	6	4.4	233	2	Q6TLZ5	Q6tlz5 mycobacteri
322	6	4.4	190	2	Q8N2X5	Q8n2x5 homo sapien	395	6	4.4	233	2	Q92Z40	Q92z40 rhizobium m
323	6	4.4	190	2	Q8GHN3	Q8ghn3 pseudomonas	396	6	4.4	233	2	Q7NGN2	Q7ngn2 gloeobacter

397	6	4.4	233	2	Q9TV64	Q9jv64	neisseria m	470	6	4.4	261	2	Q6L711	Q6l71l	buergeria b
398	6	4.4	233	2	Q9K054	Q9k054	neisseria m	471	6	4.4	261	2	Q7VSU8	Q7vsj8	bordetella
399	6	4.4	234	1	SNG1_HUMAN	Q43759	homo sapien	472	6	4.4	261	2	Q7W459	Q7w459	bordetella
400	6	4.4	234	1	SNG1_MOUSE	O55100	mus musculus	473	6	4.4	261	2	Q7WFL6	Q7wfl6	bordetella
401	6	4.4	234	1	SNG1_RAT	Q62876	rattus norv	474	6	4.4	262	2	Q9RB26	Q9rb26	peritobacter
402	6	4.4	234	2	Q26717	Q26747	methanobact	475	6	4.4	262	2	Q9XB51	Q9xb51	erwinia car
403	6	4.4	235	2	Q662B2	Q662e2	borrelia ga	476	6	4.4	262	2	Q6CZM8	Q6czm8	erwinia car
404	6	4.4	235	2	Q82KR7	Q92ky7	rhizobium m	477	6	4.4	263	2	Q6NJH0	Q6njh0	corynebacte
405	6	4.4	236	2	Q82WY9	Q8zwr9	pyrobaculum	478	6	4.4	264	2	O87202	O87202	azospirillum
406	6	4.4	236	2	Q82ZB2	Q82zb2	enterococcu	479	6	4.4	264	2	Q9HZV7	Q9hzb7	pseudomonas
407	6	4.4	239	2	Q987U4	Q987u4	rhizobium 1	480	6	4.4	265	2	Q7QQF8	Q7qqf8	giardia lam
408	6	4.4	239	2	O8D2M8	Q8d2m8	wiggleswort	481	6	4.4	265	2	O8RPD5	O8rpd5	legionella
409	6	4.4	239	2	Q9KFX5	Q9kfk5	bacillus ha	482	6	4.4	265	2	Q9PDK8	Q9pdk8	zymomonas m
410	6	4.4	240	2	O30144	Q30144	archaeoglob	483	6	4.4	265	2	Q7V3Z4	Q7v3z4	prochloroco
411	6	4.4	240	2	Q6NCC7	Q6ncc7	rhodopseudo	484	6	4.4	266	2	Q7VNX0	Q7vnx0	haemophilus
412	6	4.4	242	2	Q81JV6	Q81jv6	plasmodium	485	6	4.4	266	2	O6DC54	O6dc54	brachydanio
413	6	4.4	242	2	Q7Z0H0	Q7z0h0	plasmodium	486	6	4.4	267	2	O6CLX9	O6clx9	kluveromyc
414	6	4.4	242	2	Q82RL6	Q82rl6	streptomyce	487	6	4.4	268	1	ET1B_XENLA	P18756	xenopus lae
415	6	4.4	242	2	Q8AK12	Q8ak12	desulfotale	488	6	4.4	268	2	Q8I6J7	Q8i6j7	ciona intes
416	6	4.4	242	2	Q8BF77	Q8bf77	uncultured	489	6	4.4	269	2	Q9W4X7	Q9w4x7	drosophila
417	6	4.4	242	2	Q6RXJ0	Q6rxj0	human cytom	490	6	4.4	269	2	Q74PA9	Q74pa9	yersinia pe
418	6	4.4	242	2	Q75RX5	Q75rx5	oreochromis	491	6	4.4	269	2	Q8YBG1	Q8ybg1	brucella me
419	6	4.4	243	2	O6INE4	Q6ine4	xenopus lae	492	6	4.4	269	2	Q8YFH2	Q8yfh2	bradyrhizob
420	6	4.4	244	2	Q8WQY9	Q8wqy9	aprocallis	493	6	4.4	269	2	Q8CZF9	Q8czf9	yersinia pe
421	6	4.4	244	2	Q74K22	Q74k22	lactobacill	494	6	4.4	269	2	Q8FWY4	Q8fwy4	brucella su
422	6	4.4	245	2	Q8Y1B9	Q8y1b9	raistonia s	495	6	4.4	270	2	Q74DN6	Q74dn6	geobacter s
423	6	4.4	245	2	Q88I43	Q88i43	pseudomonas	496	6	4.4	271	2	P78731	P78731	pneumocysti
424	6	4.4	246	2	O6IWO4	Q6iwo4	burkholderi	497	6	4.4	272	2	Q9Y138	Q9y138	clostridium
425	6	4.4	246	2	Q9SY37	Q9sy37	arabidopsis	498	6	4.4	273	2	Q9Y1G6	Q9y1g6	columbid ci
426	6	4.4	246	2	Q8RGB2	Q8rgb2	fusobacteri	499	6	4.4	273	2	O91GA1	O91ga1	columbid ci
427	6	4.4	246	2	O6NGD2	Q6ngd2	corynebacte	500	6	4.4	273	2	Q9IG42	Q9ig42	columbid ci
428	6	4.4	246	2	Q9NFV3	Q9nfv3	gloeobacter	501	6	4.4	274	1	GADX_ECO27	Q9eyv5	escherichia
429	6	4.4	247	1	Y125_RICPR	P41087	rickettsia	502	6	4.4	274	1	GADX_ECO57	P58220	escherichia
430	6	4.4	247	1	Y167_RICCN	Q92ja0	rickettsia	503	6	4.4	274	1	GADX_ECOL6	Q8fcf6	escherichia
431	6	4.4	247	2	Q7PAR7	Q7par7	rickettsia	504	6	4.4	274	1	GADX_ECOL6	P37639	escherichia
432	6	4.4	247	2	O8PPL6	Q8ppl6	xanthomonas	505	6	4.4	274	1	GADX_SHIFL	Q83pr0	shigella fl
433	6	4.4	247	2	Q68XP2	Q68xp2	rickettsia	506	6	4.4	274	1	THCF_RHOER	O05691	rhodococcus
434	6	4.4	247	2	Q9KFL0	Q9kfl0	bacillus ha	507	6	4.4	275	2	Q6ML97	Q6ml97	bdellovibri
435	6	4.4	247	2	Q8BF96	Q8bf96	uncultured	508	6	4.4	275	2	Q9CCW0	Q9ccw0	mycobacteri
436	6	4.4	248	1	GRPE_ANASP	Q9yua7	anabaena sp	509	6	4.4	276	2	O6Z9X5	Q6z9x5	oryza sativ
437	6	4.4	248	2	Q95438	Q95438	pseudomonas	510	6	4.4	276	2	Q737L6	Q737l6	bacillus ce
438	6	4.4	248	2	O73ECO	Q73ec0	bacillus ce	511	6	4.4	277	2	O86ZC6	O86zc6	gibberella
439	6	4.4	248	2	O91314	Q91314	pseudomonas	512	6	4.4	277	2	O53640	O53640	streptococc
440	6	4.4	249	2	Q6D4F3	Q6d4p3	erwinia car	513	6	4.4	277	2	Q887P6	Q887p6	pseudomonas
441	6	4.4	249	2	Q8UJ50	Q8uj50	agrobacteri	514	6	4.4	277	2	Q8DYF6	Q8dyf6	streptococc
442	6	4.4	250	2	Q636V7	Q636v7	bacillus ce	515	6	4.4	277	2	Q8DZN3	Q8dzn3	streptococc
443	6	4.4	250	2	Q9YMY8	Q9ymy8	anabaena sp	516	6	4.4	277	2	O8FPY2	O8fpv2	corynebacte
444	6	4.4	250	2	O733B4	Q733b4	bacillus ce	517	6	4.4	278	1	BMRR_BACSU	P39075	bacillus su
445	6	4.4	250	2	O81A69	Q81a69	bacillus ce	518	6	4.4	278	2	O64773	O64773	arabidopsis
446	6	4.4	250	2	Q81WM6	Q81w6	bacillus an	519	6	4.4	278	2	Q40768	Q40768	prunus dulc
447	6	4.4	250	2	Q6HF92	Q6hf92	bacillus th	520	6	4.4	280	2	Q8PI45	Q8pi45	xanthomonas
448	6	4.4	251	2	Q663S0	Q663s0	yersinia ps	521	6	4.4	281	2	O64NU1	O64nu1	bacteroides
449	6	4.4	251	2	Q8Z9T6	Q8z9t6	yersinia pe	522	6	4.4	282	2	O8TJZ1	O8tjz1	methanosarc
450	6	4.4	252	2	O7P501	Q7p501	fusobacteri	523	6	4.4	282	2	O74BQ6	O74bq6	geobacter s
451	6	4.4	252	2	Q8RH62	Q8rh62	fusobacteri	524	6	4.4	283	2	Q9AA26	Q9aa26	caulobacter
452	6	4.4	253	2	Q7YU02	Q7yu02	sulfolobus	525	6	4.4	285	2	Q97UF4	Q97uf4	sulfolobus
453	6	4.4	253	2	Q70MM8	Q70mm8	crassostrea	526	6	4.4	286	2	O53710	O53710	mycobacteri
454	6	4.4	254	2	Q9UF65	Q9uf65	homo sapien	527	6	4.4	286	2	O7U252	O7u252	mycobacteri
455	6	4.4	255	2	O78727	P78727	pneumocysti	528	6	4.4	286	2	Q9K7Q6	Q9k7q6	caeniorhabdi
456	6	4.4	255	2	O6NLM6	O6nlm6	drosophila	529	6	4.4	287	2	O6TMY7	O6tmv7	hyphomonas
457	6	4.4	255	2	O68049	O68049	rhodobacter	530	6	4.4	287	2	Q8PNB7	Q8pnb7	xanthomonas
458	6	4.4	255	2	Q88NR7	Q88nr7	pseudomonas	531	6	4.4	287	2	Q9CHQ9	Q9chq9	lactococcus
459	6	4.4	256	2	Q95Z09	Q95z09	trypaenoma	532	6	4.4	287	2	Q6DFS0	Q6df80	xenopus tro
460	6	4.4	256	2	O7PE56	Q7pe56	anopheles g	533	6	4.4	288	2	Q9XUZ4	Q9xuz4	caenorhabdi
461	6	4.4	256	2	Q9DXV5	Q9dxv5	tomato spot	534	6	4.4	289	2	O8YSU1	O8ysu1	anabaena sp
462	6	4.4	257	1	DLHH_SULSO	P95862	sulfolobus	535	6	4.4	289	2	Q9J5E0	Q9j5e0	fowlpox vir
463	6	4.4	258	2	Q8FY43	Q8fy43	brucella su	536	6	4.4	290	1	EX05_BPT5	P06229	bacterioph
464	6	4.4	259	2	Q92KZ5	Q92kz5	rhizobium m	537	6	4.4	291	1	Y620_METJA	O58037	methanococc
465	6	4.4	260	2	Q6BQC2	Q6bqc2	debaryomyce	538	6	4.4	292	1	MDCB_ACICA	Q59033	acinetobact
466	6	4.4	260	2	Q7VM79	Q7vm79	haemophilus	539	6	4.4	292	2	Q8LAG0	Q8lag0	arabidopsis
467	6	4.4	261	2	Q96XK4	Q96xk4	sulfolobus	540	6	4.4	292	2	Q9FWT1	Q9fw1	arabidopsis
468	6	4.4	261	2	P78729	P78729	pneumocysti	541	6	4.4	292	2	Q9FY94	Q9fy94	arabidopsis
469	6	4.4	261	2	Q94YM6	Q94ym6	rana nigrom	542	6	4.4	293	1	YFIE_ECOLI	P33634	escherichia

543	6	4.4	293	2	Q72JW2	Q72jw2 thermus the	616	6	4.4	315	2	Q6E298	Q6e298 arabidopsis
544	6	4.4	294	2	Q94E53	Q94e53 oryza sativ	617	6	4.4	315	2	Q9FX92	Q9fx92 arabidopsis
545	6	4.4	294	2	Q9FW23	Q9fw23 arabidopsis	618	6	4.4	315	2	Q8CNA0	Q8cna0 staphylococ
546	6	4.4	294	2	Q8P7C3	Q8p7c3 xanthomonas	619	6	4.4	316	2	O58654	O58654 pyrococcus
547	6	4.4	294	2	Q8P1P6	Q8p1p6 xanthomonas	620	6	4.4	316	2	O85VX4	O85vx4 manheimia
548	6	4.4	295	2	Q2O811	Q2o811 caenorhabdi	621	6	4.4	316	2	Q88121	Q88121 pseudomonas
549	6	4.4	295	2	Q8PAE8	Q8pae8 xanthomonas	622	6	4.4	316	2	Q9PNG1	Q9pn61 campylobact
550	6	4.4	296	1	MALG_ECOS7	P68185 escherichia	623	6	4.4	317	2	Q738B9	Q738b9 bacillus ce
551	6	4.4	296	1	MALG_ECOL6	P68184 escherichia	624	6	4.4	318	2	Q7R9B3	Q7r9b3 plasmodium
552	6	4.4	296	1	MALG_ECOLI	P68183 escherichia	625	6	4.4	318	2	Q8GTW7	Q8gtm7 oryza sativ
553	6	4.4	296	1	MALG_ENTAB	P18814 enterobacte	626	6	4.4	318	2	Q9RHT5	Q9rht5 streptomyce
554	6	4.4	296	1	MALG_PHOIL	Q7n983 photorhabdu	627	6	4.4	318	2	Q8ZCH1	Q8zch1 streptomyce
555	6	4.4	296	1	MALG_SALTY	Q8zlu3 salmonella	628	6	4.4	318	2	Q89XX4	Q89xx4 bradyrhizob
556	6	4.4	296	1	MALG_SALTY	P26468 salmonella	629	6	4.4	318	2	Q9KVD3	Q9kvd3 vibrio chol
557	6	4.4	296	1	MALG_SHIFL	P68186 shigella fl	630	6	4.4	318	2	Q9PM73	Q9pm73 campylobact
558	6	4.4	296	2	O6CD51	O6cd51 yarrowia li	631	6	4.4	319	2	O8S629	O8s629 oryza sativ
559	6	4.4	296	2	Q664X1	Q664x1 yersinia ps	632	6	4.4	319	2	Q83X38	Q8x38 streptomyce
560	6	4.4	297	2	Q7VIG3	Q7vig3 helicobacte	633	6	4.4	319	2	Q7MT26	Q7mt26 porphyromon
561	6	4.4	297	2	Q9A589	Q9a589 pseudomonas	634	6	4.4	320	2	O06996	O06996 bacillus su
562	6	4.4	297	2	Q9HX00	Q9hx00 pseudomonas	635	6	4.4	320	2	Q97GF5	Q97gf5 clostridium
563	6	4.4	297	2	O8QX00	O8qx00 garlic late	636	6	4.4	320	2	Q73M86	Q73m86 treponema d
564	6	4.4	297	2	O8UZA2	O8uza2 garlic late	637	6	4.4	321	2	O67QA9	Q67qa9 symbiobacte
565	6	4.4	298	2	Q8X121	Q8x121 pneumocysti	638	6	4.4	321	2	Q986M3	Q986m3 rhizobium l
566	6	4.4	299	2	Q8ZMX6	Q8zmx6 salmonella	639	6	4.4	321	2	Q8R310	Q8r310 mus musculu
567	6	4.4	299	2	Q7MR96	Q7mr96 wolinnella s	640	6	4.4	322	2	Q983C4	Q983c4 rhizobium l
568	6	4.4	300	2	Q9VDJ3	Q9vdj3 drosophila	641	6	4.4	322	2	Q8JFW6	Q8jfw6 brachydanio
569	6	4.4	300	2	Q7D9X3	Q7d9x3 mycobacteri	642	6	4.4	323	2	O6KZU0	O6kzu0 picrophilus
570	6	4.4	300	2	P96811	P96811 mycobacteri	643	6	4.4	323	2	O650S2	O650s2 bacteroides
571	6	4.4	300	2	Q8ARY6	Q8ary6 deusulfotale	644	6	4.4	323	2	Q99XV0	Q99xv0 bradyrhizob
572	6	4.4	300	2	Q9E7N7	Q9e7n7 lettuce nec	645	6	4.4	324	2	Q9UUP4	Q9uup4 pneumocysti
573	6	4.4	301	2	O26437	O26437 methanobact	646	6	4.4	324	2	Q738W6	Q738w6 bacillus ce
574	6	4.4	301	2	O65H73	O65h73 bacillus li	647	6	4.4	324	2	Q81RL2	Q81rl2 bacillus an
575	6	4.4	301	2	O65H73	O65h73 bacillus li	648	6	4.4	324	2	O6HJB5	O6hjb5 bacillus th
576	6	4.4	301	2	O89PG1	O89pg1 bradyrhizob	649	6	4.4	325	2	O7VZT6	O7vzt6 bordetella
577	6	4.4	303	1	MALG_YERPE	Q74rf8 yersinia pe	650	6	4.4	325	2	Q7WS74	Q7ws74 bordetella
578	6	4.4	303	2	Q8EUG3	Q8eug3 oryza sativ	651	6	4.4	325	2	Q7WCQ4	Q7wcq4 bordetella
579	6	4.4	303	2	Q9K3X6	Q9k3x6 streptomyce	652	6	4.4	325	2	Q7ZZ64	Q7zz64 brachydanio
580	6	4.4	303	2	Q7Z263	Q7z263 brachydanio	653	6	4.4	326	1	VP40_EBOZM	Q00030 equine herp
581	6	4.4	304	1	ASPA_PROMM	Q7v516 prochloroco	654	6	4.4	326	1	VP40_EBOZM	Q00030 ebola virus
582	6	4.4	304	2	Q8EIN6	Q8ein6 shewanella	655	6	4.4	326	2	Q92Z59	Q92zr9 rhizobium m
583	6	4.4	305	1	FMT_CAMJE	Q9pj28 campylobact	656	6	4.4	326	2	Q81DZ5	Q81dz5 streptomyce
584	6	4.4	305	2	P72579	P72579 sulfolobus	657	6	4.4	326	2	Q829K7	Q829k7 streptomyce
585	6	4.4	305	2	Q96Y68	Q96y68 sulfolobus	658	6	4.4	326	2	O39251	O39251 equid herpe
586	6	4.4	305	2	O32796	Q32796 lactococcus	659	6	4.4	326	2	O913A4	Q913a4 zaire ebola
587	6	4.4	305	2	O32798	O32798 lactococcus	660	6	4.4	326	2	O77DJ6	Q77dj6 zaire ebola
588	6	4.4	305	2	Q7ND98	Q7nd98 gloebacter	661	6	4.4	327	2	Q9M6R7	Q9m6r7 psium sativ
589	6	4.4	305	2	Q835V5	Q835v5 enterococcu	662	6	4.4	327	2	Q8UJL3	Q8ujl3 agrobacteri
590	6	4.4	305	2	Q9L259	Q9l259 streptomyce	663	6	4.4	328	1	ABF2_STRCX	P82594 streptomyce
591	6	4.4	306	1	EXTN_DAUCA	P06599 daucus caro	664	6	4.4	328	1	NC5R_ARATH	P82591 arabidopsis
592	6	4.4	307	1	YMC1_YEAST	P32131 saccharomyc	665	6	4.4	328	2	Q9D7H2	Q9d7h2 mus musculu
593	6	4.4	307	2	O61QC7	O61qc7 brachydanio	666	6	4.4	329	2	O18071	O18071 caenorhabdi
594	6	4.4	308	2	Q8FF12	Q8ff12 escherichia	667	6	4.4	329	2	Q9MFE7	Q9mfe7 beta vulgar
595	6	4.4	308	2	Q83Q11	Q83q11 shigella fl	668	6	4.4	329	2	Q92TI6	Q92ti6 rhizobium m
596	6	4.4	308	2	Q8X5A8	Q8x5a8 escherichia	669	6	4.4	329	2	Q80PX1	Q80px1 human herpe
597	6	4.4	309	2	Q96EJ8	Q96ej8 homo sapien	670	6	4.4	329	2	Q80PX2	Q80px2 human herpe
598	6	4.4	309	2	Q86X20	Q86x20 homo sapien	671	6	4.4	329	2	Q80PX3	Q80px3 human herpe
599	6	4.4	309	2	Q7MPZ7	Q7mpz7 vibrio vuln	672	6	4.4	329	2	Q80PX4	Q80px4 human herpe
600	6	4.4	309	2	Q7NOA8	Q7noa8 photorhabdu	673	6	4.4	329	2	Q80PX5	Q80px5 human herpe
601	6	4.4	310	1	CNJC_TETTH	P16925 tetrahymena	674	6	4.4	330	2	O76852	O76852 tetrahymena
602	6	4.4	310	2	P96562	P96562 amycollatops	675	6	4.4	330	2	Q41402	Q41402 sesbania ro
603	6	4.4	311	2	O44984	O44984 caenorhabdi	676	6	4.4	331	1	LDHD_LEUMC	P51011 leuconostoc
604	6	4.4	311	2	Q87UM8	Q87um8 pseudomonas	677	6	4.4	331	2	O6ZFU6	O6zfu6 oryza sativ
605	6	4.4	312	1	Y531_METTH	O26631 methanobact	678	6	4.4	331	2	O83359	O83359 treponema p
606	6	4.4	312	2	Q87L11	Q87l11 listeria mo	679	6	4.4	331	2	Q9JIT7	Q9jit7 cavia porce
607	6	4.4	312	2	Q720F6	Q720f6 listeria mo	680	6	4.4	331	2	Q8JXP9	Q8jpx9 reston ebol
608	6	4.4	312	2	Q895S8	Q895s8 clostridium	681	6	4.4	332	2	Q96ZS5	Q96zss sulfolobus
609	6	4.4	313	2	O25523	O25523 helicobacte	682	6	4.4	332	2	Q84I39	Q84i39 helicobacte
610	6	4.4	313	2	O8Y556	Q8y556 listeria mo	683	6	4.4	332	2	O6M9Z5	O6m9z5 parachlamyd
611	6	4.4	313	2	Q71XE5	Q71xe5 listeria mo	684	6	4.4	333	2	O81494	O81494 arabidopsis
612	6	4.4	313	2	Q9KA02	Q9ka02 bacillus ha	685	6	4.4	333	2	Q87G77	Q87gy7 vibrio para
613	6	4.4	313	2	Q9ZK24	Q9zk24 helicobacte	686	6	4.4	333	2	Q9JS73	Q9js73 chlamydia p
614	6	4.4	314	1	HEM3_BRUME	Q8yjb0 bruceella me	687	6	4.4	333	2	Q9Z6L1	Q9z6l1 chlamydia p
615	6	4.4	314	1	HEM3_BRUSU	Q8fyi6 bruceella su	688	6	4.4	334	1	PURR_PASMU	Q9cn88 pasteurella

689	6	4.4	334	2	O45307	O45307 caenorhabdi
690	6	4.4	335	2	Q9UZM6	Q9uzm6 pyrococcus
691	6	4.4	336	2	Q7PWN4	Q7pwn4 anopheles g
692	6	4.4	337	1	XRC4 HUMAN	Q13426 homo sapien
693	6	4.4	338	2	Q67MQ8	Q67mq8 symbiobacte
694	6	4.4	339	2	Q84I37	Q84i37 helicobacte
695	6	4.4	340	2	O58840	O58840 pyrococcus
696	6	4.4	341	2	Q8U204	Q8u204 pyrococcus
697	6	4.4	342	2	Q75LX7	Q75lx7 oryza sativ
698	6	4.4	343	2	Q84I35	Q84i35 helicobacte
699	6	4.4	344	2	Q73XD2	Q73xd2 mycobacteri
700	6	4.4	345	2	Q89GY5	Q89gy5 bradyrhizob
701	6	4.4	346	2	Q7MXV9	Q7mxy9 porphyromon
702	6	4.4	347	2	Q6VZQ0	Q6vzq0 canarypox v
703	6	4.4	348	2	Q6C875	Q6c875 yarrowia li
704	6	4.4	349	2	Q69J25	Q69j25 oryza sativ
705	6	4.4	350	2	Q89AQC	Q89aq4 bacteroides
706	6	4.4	351	2	O6YCH1	O6ych1 mus musculu
707	6	4.4	352	2	Q8LMT1	Q8lmt1 arabidopsis
708	6	4.4	353	2	Q8MPL1	Q8mpl1 bdellovibri
709	6	4.4	354	2	Q7T5J0	Q7t5j0 cryptophleb
710	6	4.4	355	2	Q93KV2	Q93kv2 streptomyce
711	6	4.4	356	2	Q66IY2	Q66iy2 xenopus lae
712	6	4.4	357	2	Q6DFO7	Q6dfq7 xenopus tro
713	6	4.4	358	2	Q84I34	Q84i34 helicobacte
714	6	4.4	359	2	Q8Y4I4	Q8y4i4 listeria mo
715	6	4.4	360	2	Q927H6	Q927h6 listeria in
716	6	4.4	361	2	Q7IWA8	Q7iwa8 listeria mo
717	6	4.4	362	1	PILT_PSEAE	P24559 pseudomonas
718	6	4.4	363	2	Q7BTG5	Q7btg5 pseudomonas
719	6	4.4	364	2	Q8F667	Q8f667 pseudomonas
720	6	4.4	365	2	Q87CD4	Q87cd4 xylella fas
721	6	4.4	366	2	Q87V94	Q87v94 pseudomonas
722	6	4.4	367	2	Q9PCX1	Q9pcx1 xylella fas
723	6	4.4	368	1	ADD_RALSO	Q8xxl5 ralstonia s
724	6	4.4	369	1	CYSA_VIBU	Q8d653 vibrio vuln
725	6	4.4	370	1	VAOD_YEAST	P32366 saccharomyc
726	6	4.4	371	2	Q8NL23	Q8nl23 xanthomonas
727	6	4.4	372	2	Q7CLR1	Q7clr1 xanthomonas
728	6	4.4	373	2	Q7PLN4	Q7pln4 chromobacte
729	6	4.4	374	1	LUXA_PHOPO	P24113 photobacter
730	6	4.4	375	2	Q97ZH7	Q97zh7 sulfolobus
731	6	4.4	376	2	Q7WP94	Q7wp94 bordetella
732	6	4.4	377	2	Q89LP2	Q89lp2 bradyrhizob
733	6	4.4	378	2	Q9RW82	Q9rwh2 deinococcus
734	6	4.4	379	2	Q8ZSW1	Q8zsw1 pyrobaculum
735	6	4.4	380	2	Q756V5	Q756v5 ashbya goss
736	6	4.4	381	2	Q8P334	Q8p334 xanthomonas
737	6	4.4	382	2	Q8XV23	Q8xv23 ralstonia s
738	6	4.4	383	2	Q8A6V2	Q8a6v2 proptonibac
739	6	4.4	384	2	Q72M10	Q72m10 leptospira
740	6	4.4	385	2	Q8A2H5	Q8a2h5 bacteroides
741	6	4.4	386	2	O18110	O18110 caenorhabdi
742	6	4.4	387	2	Q86JV0	Q86jv0 dictyosteli
743	6	4.4	388	2	O56302	O56302 thermococcu
744	6	4.4	389	2	Q8XUC5	Q8xuc5 caenorhabdi
745	6	4.4	390	2	Q8LEX1	Q8lex1 arabidopsis
746	6	4.4	391	2	Q93Z83	Q93z83 arabidopsis
747	6	4.4	392	2	Q9STW1	Q9stn1 arabidopsis
748	6	4.4	393	2	Q9ZUB9	Q9zub9 arabidopsis
749	6	4.4	394	2	Q7UPP7	Q7upp7 rhodopirell
750	6	4.4	395	2	O81493	O81493 arabidopsis
751	6	4.4	396	2	Q944K0	Q944k0 arabidopsis
752	6	4.4	397	1	CYAB_STIAU	P40138 stigmatella
753	6	4.4	398	2	Q6BMG5	Q6bmgs debaryomyce
754	6	4.4	399	2	Q6ZOV7	Q6zov7 oryza sativ
755	6	4.4	400	2	O84I38	O84i38 helicobacte
756	6	4.4	401	2	Q8NR93	Q8nr93 corynebacte
757	6	4.4	402	2	Q7NVJ9	Q7nvj9 chromobacte
758	6	4.4	403	2	P78930	P78930 schizosacch
759	6	4.4	404	2	Q74FZ0	Q74fz0 geobacter s
760	6	4.4	405	2	Q9DF34	Q9df34 brachydanio
761	6	4.4	406	2	Q8C2A6	Q8c2a6 mus musculu

762	6	4.4	358	2	Q6UDM3	Q6udm3 psittacid h
763	6	4.4	359	1	AROB_CHRVO	Q7nz4 chromobacte
764	6	4.4	360	1	HFE_MOUSE	Q70387 mus musculu
765	6	4.4	361	1	Q6N3V1	Q6n3v1 rhodopseudo
766	6	4.4	362	2	Q8EYI5	Q8eyi5 leptospira
767	6	4.4	363	2	Q9D754	Q9d754 mus musculu
768	6	4.4	364	2	Q8T376	Q8t376 meloidogyne
769	6	4.4	365	1	ASG2_YEAST	P1163 saccharomyc
770	6	4.4	366	2	Q6Q5K8	Q6q5k8 saccharomyc
771	6	4.4	367	2	Q6Q5K9	Q6q5k9 saccharomyc
772	6	4.4	368	2	Q7AH88	Q7ah88 escherichia
773	6	4.4	369	2	Q6F7E5	Q6f7e5 acinetobact
774	6	4.4	370	2	Q9NVJ6	Q9nvj6 homo sapien
775	6	4.4	371	2	Q9RKQ5	Q9rkq5 streptomyce
776	6	4.4	372	2	Q6A6V5	Q6a6v5 propionibac
777	6	4.4	373	1	AROB_PSEPK	Q88cv2 pseudomonas
778	6	4.4	374	2	Q8X6B9	Q8x6b9 escherichia
779	6	4.4	375	1	AROB_PSESM	Q87v15 pseudomonas
780	6	4.4	376	2	Q6RCI2	Q8rci2 mycobacteri
781	6	4.4	377	2	Q7MWZ4	Q7mwz4 porphyromon
782	6	4.4	378	2	Q6ZQ44	Q6zq44 mus musculu
783	6	4.4	379	2	AROB_PSEAE	P34002 pseudomonas
784	6	4.4	380	1	HI82_PSEAE	Q9hz68 pseudomonas
785	6	4.4	381	2	Q84I36	Q84i36 helicobacte
786	6	4.4	382	2	Q6NIM2	Q6nim2 corynebacte
787	6	4.4	383	1	HUPK_RHLIV	P28153 rhizobium l
788	6	4.4	384	2	Q6BRJ2	Q6brj2 debaryomyce
789	6	4.4	385	2	Q7QQ57	Q7qq57 giardia lam
790	6	4.4	386	2	Q916T2	Q916t2 pseudomonas
791	6	4.4	387	2	Q93NC0	Q93nc0 myxococcus
792	6	4.4	388	2	Q67JF5	Q67jf5 symbiobacte
793	6	4.4	389	2	DNAB_BACSU	P17631 bacillus su
794	6	4.4	390	2	Q8YUA9	Q8yua9 anabaena sp
795	6	4.4	391	2	Q8P402	Q8p402 xanthomonas
796	6	4.4	392	2	Q8P402	Q8p402 xanthomonas
797	6	4.4	393	2	Q9PTL7	Q9ptl7 xenopus lae
798	6	4.4	394	1	Y5D9_GLOVI	Q7ndu3 gloebacter
799	6	4.4	395	2	Q9Y8P6	Q9y8p6 aeropyrum p
800	6	4.4	396	2	Q67L31	Q67l31 symbiobacte
801	6	4.4	397	2	Q6D5Y0	Q6d5y0 erwinia car
802	6	4.4	398	2	Q37387	Q37387 common chim
803	6	4.4	399	2	Q80IS9	Q80is9 xenopus lae
804	6	4.4	400	2	Q8GHV5	Q8ghv5 pseudomonas
805	6	4.4	401	2	FLIY_BACSU	P24073 bacillus su
806	6	4.4	402	2	Q7XZAO	Q7x2ao pseudomonas
807	6	4.4	403	2	Q6CHZ1	Q6chz1 yarrowia li
808	6	4.4	404	2	Q73R97	Q73r97 treponema d
809	6	4.4	405	2	Q9K000	Q9k000 neisseria m
810	6	4.4	406	1	ARGE_BUCAI	P57155 buchera ap
811	6	4.4	407	2	Q8BIM3	Q8bim3 mus musculu
812	6	4.4	408	2	Q6Y2P9	Q6y2p9 oryza sativ
813	6	4.4	409	2	Q9EX13	Q9ex13 streptomyce
814	6	4.4	410	2	ARGJ_CORDI	P62059 corynebacte
815	6	4.4	411	2	CUE1_HUMAN	Q9nmw3 homo sapien
816	6	4.4	412	2	Q7PK57	Q7pk57 anopheles g
817	6	4.4	413	2	Q64094	Q64094 bacterioph
818	6	4.4	414	2	O31927	O31927 bacillus su
819	6	4.4	415	2	Q6FEJ4	Q6fej4 acinetobact
820	6	4.4	416	2	Q98J75	Q98j75 rhizobium l
821	6	4.4	417	2	CUE1_MOUSE	Q8r3v6 mus musculu
822	6	4.4	418	2	Q8ZYV9	Q8zyv9 pyrobaculum
823	6	4.4	419	2	Q96Z16	Q96z16 sulfolobus
824	6	4.4	420	2	O16881	O16881 caenorhabdi
825	6	4.4	421	2	Q8KE01	Q8ke01 chlorobium
826	6	4.4	422	2	Q6LXW7	Q6lwx7 methanococc
827	6	4.4	423	2	Q6N4F5	Q6n4f5 rhodopseudo
828	6	4.4	424	2	Q89IU8	Q89iu8 bradyrhizob
829	6	4.4	425	2	Q8DJV0	Q8djv0 synechococc
830	6	4.4	426	2	Q22101	Q22101 caenorhabdi
831	6	4.4	427	1	PCL_ECTHA	P42516 ectothiorho
832	6	4.4	428	2	Q7JNC6	Q7jnc6 drosophila
833	6	4.4	429	2	Q7QG74	Q7qg74 anopheles g
834	6	4.4	430	2	Q02690	Q02690 podospora a

835	6	4.4	391	2	Q8D5A1	Q8d5a1 vibrio vuln	908	6	4.4	419	2	Q73F05	Q73f05 bacillus ce
836	6	4.4	392	1	LXC1_YARLI	P41929 yarrowia li	909	6	4.4	419	2	Q8FQ06	Q8fq06 corynebacte
837	6	4.4	392	2	Q629Y0	Q629y0 oryza sativ	910	6	4.4	419	2	Q6HPJ5	Q6hpj5 bacillus th
838	6	4.4	392	2	Q8GALO	Q8gal0 arthrobacte	911	6	4.4	420	2	Q8PVS6	Q8pvs6 methanosarc
839	6	4.4	393	2	Q7Y0Z8	Q7y0z8 lycopersico	912	6	4.4	420	2	Q6X8L3	Q6x8l3 homo sapien
840	6	4.4	393	2	Q8RR83	Q8rr83 acetobacter	913	6	4.4	420	2	Q86UN3	Q8eun3 homo sapien
841	6	4.4	393	2	Q921D8	Q921d8 mus musculu	914	6	4.4	420	2	Q7WE84	Q7we84 bordetella
842	6	4.4	394	2	Q6M2Z0	Q6m2z0 methylocyst	915	6	4.4	420	2	Q83A86	Q83a86 coxiella bu
843	6	4.4	394	2	Q8REK6	Q8ren6 fusobacteri	916	6	4.4	420	2	Q6AET0	Q6aet0 leifsonia x
844	6	4.4	394	2	Q6A5K4	Q6a5k4 propionibac	917	6	4.4	421	2	Q9SX61	Q9sx61 arabidopsis
845	6	4.4	394	2	Q7VVV1	Q7vvv1 bordetella	918	6	4.4	422	1	PROA_NITEU	Q820i7 nitrosomona
846	6	4.4	394	2	Q7WKL9	Q7wkl9 bordetella	919	6	4.4	423	2	Q70IN2	Q70in2 pseudomonas
847	6	4.4	394	2	Q9KB99	Q9kb99 bacillus ha	920	6	4.4	423	2	Q63BU5	Q63bu5 bacillus ce
848	6	4.4	395	2	Q7XEG1	Q7xeg1 oryza sativ	921	6	4.4	424	2	Q6F735	Q6f735 acinetobact
849	6	4.4	395	2	Q6EVS8	Q6evs8 versinia ps	922	6	4.4	424	2	Q7UL99	Q7ul99 rhodopirell
850	6	4.4	395	2	Q9KZC2	Q9kzc2 streptomyce	923	6	4.4	425	2	Q76652	Q76652 caenorhabdi
851	6	4.4	396	2	Q8BJ17	Q8bj17 debaryomyce	924	6	4.4	425	2	Q6JT24	Q6jtt24 ornithocton
852	6	4.4	397	2	Q9UAU3	Q9uau3 caenorhabdi	925	6	4.4	428	2	Q8NAB8	Q8nab8 homo sapien
853	6	4.4	398	2	Q978Z4	Q978z4 thermoplasm	926	6	4.4	429	1	MANA_CANGA	Q761q2 candida gla
854	6	4.4	398	2	Q05765	Q05765 saccharomyc	927	6	4.4	429	2	Q8SS48	Q8ss48 encaphalito
855	6	4.4	398	2	Q63R97	Q63r97 burkholderi	928	6	4.4	430	2	Q97AH4	Q97ah4 thermoplasm
856	6	4.4	399	2	Q9HGN6	Q9hgn6 schizosacch	929	6	4.4	430	2	Q7ML61	Q7ml61 vibrio vuln
857	6	4.4	399	2	Q8L912	Q8l912 arabidopsis	930	6	4.4	430	2	Q8A5C0	Q8a5c0 bacteroides
858	6	4.4	399	2	Q9M9V4	Q9m9v4 arabidopsis	931	6	4.4	431	1	FAAA_EMENI	Q00770 emeritella
859	6	4.4	400	2	Q9GZHV	Q9gzhv caenorhabdi	932	6	4.4	431	2	Q7MTJ6	Q7mtj6 porphyronon
860	6	4.4	400	2	Q6N8Z6	Q6n8z6 rhodopsendo	933	6	4.4	431	2	Q7TU40	Q7tu40 prochloroco
861	6	4.4	400	2	Q73ND4	Q73nd4 treponema d	934	6	4.4	432	2	Q94C40	Q94c40 arabidopsis
862	6	4.4	400	2	Q6P6Q1	Q6p6q1 mus musculu	935	6	4.4	432	2	Q9X804	Q9x804 streptomyce
863	6	4.4	401	2	Q886E3	Q886e3 rhizobium l	936	6	4.4	433	1	HTR2_HALVA	P42258 haloarcula
864	6	4.4	401	2	Q7U8J2	Q7u8j2 synechococc	937	6	4.4	433	2	Q8YNO2	Q8ynq2 anabaena sp
865	6	4.4	402	2	Q8KE54	Q8ke54 chlorobium	938	6	4.4	433	2	Q7V019	Q7v019 prochloroco
866	6	4.4	402	2	Q7V4M1	Q7v4m1 prochloroco	939	6	4.4	433	2	Q9A3S6	Q9a3s6 caulobacter
867	6	4.4	402	2	Q6D669	Q6d669 erwinia car	940	6	4.4	434	2	Q07364	Q07364 chlamydia t
868	6	4.4	402	2	Q8W529	Q8w529 fugu rubrip	941	6	4.4	434	2	Q84099	Q84099 chlamydia t
869	6	4.4	403	2	Q742P6	Q742p6 mycobacteri	942	6	4.4	434	2	Q823F1	Q823f1 chlamydyphi
870	6	4.4	404	2	Q7QY67	Q7qy67 giardia lam	943	6	4.4	434	2	Q9PKT9	Q9pkt9 chlamydia m
871	6	4.4	404	2	Q7MC72	Q7mc72 vibrio vuln	944	6	4.4	434	2	Q9Z8M2	Q9z8m2 chlamydia p
872	6	4.4	405	2	Q7QZT8	Q7qzt8 sulfobolus	945	6	4.4	436	1	RSMB_PSBPK	Q88rr3 pseudomonas
873	6	4.4	405	2	Q9AXJ7	Q9axj7 medicago tr	946	6	4.4	436	2	Q68604	Q68604 brevibacter
874	6	4.4	406	1	C5C4_AMYOR	Q8rn03 amycolatops	947	6	4.4	438	1	ET1A_XENLA	P18755 xenopus lae
875	6	4.4	406	2	Q94IES	Q94ies cyanidiosch	948	6	4.4	438	2	Q64CT2	Q64ct2 uncultured
876	6	4.4	407	2	Q6CQN8	Q6ccn8 kluveromyc	949	6	4.4	438	2	Q50175	Q50175 mycobacteri
877	6	4.4	407	2	Q6NCV1	Q6ncv1 rhodopsendo	950	6	4.4	439	2	Q9V0P1	Q9v0p1 pyrococcus
878	6	4.4	409	2	Q7PS28	Q7ps28 anopheles g	951	6	4.4	439	2	Q872D8	Q872d8 neurospora
879	6	4.4	409	2	Q65ZT1	Q65zt1 borrelia ga	952	6	4.4	439	2	Q6DJL5	Q6djl5 xenopus lae
880	6	4.4	410	2	Q6JKT4	Q6jkt4 zoothermopsi	953	6	4.4	440	1	ETSI_MOUSE	P27577 mus musculu
881	6	4.4	410	2	Q6JKT7	Q6jkt7 zoothermopsi	954	6	4.4	440	2	Q50114	Q50114 pyrococcus
882	6	4.4	410	2	Q9AHF3	Q9ahf3 lysobacter	955	6	4.4	440	2	Q8VKH9	Q8vkh9 mycobacteri
883	6	4.4	411	2	Q9YCT5	Q9yct5 aeropyrum p	956	6	4.4	440	2	Q8Y490	Q8y490 listeria mo
884	6	4.4	411	2	Q7PT10	Q7pt10 anopheles g	957	6	4.4	440	2	Q927S8	Q927s8 listeria in
885	6	4.4	411	2	Q7W783	Q7w783 bordetella	958	6	4.4	440	2	Q71WL4	Q71wl4 listeria mo
886	6	4.4	412	2	Q8N6E0	Q8ne60 homo sapien	959	6	4.4	440	2	Q8BVW8	Q8bv8 mus musculu
887	6	4.4	413	2	Q8HEJ0	Q8hej0 neurospora	960	6	4.4	441	1	ETSI_HUMAN	P14921 homo sapien
888	6	4.4	413	2	Q9NAL6	Q9nal6 caenorhabdi	961	6	4.4	441	1	ETSI_RAT	P41156 rattus norv
889	6	4.4	414	2	Q6LPK3	Q6lpk3 photobacter	962	6	4.4	441	1	ETSA_CHICK	P13474 gallus gall
890	6	4.4	414	2	Q7V099	Q7v099 prochloroco	963	6	4.4	441	2	Q6FG54	Q6fg54 homo sapien
891	6	4.4	415	2	Q8LP50	Q8lp50 lunaria ann	964	6	4.4	441	2	Q6Q428	Q6q428 oryctolagus
892	6	4.4	415	2	Q8SGB2	Q8sgb2 uncultured	965	6	4.4	441	2	Q69408	Q69408 eubacterium
893	6	4.4	415	2	Q7W0P6	Q7w0p6 bordetella	966	6	4.4	441	2	Q85376	Q85376 proteus mir
894	6	4.4	415	2	Q7W3F8	Q7w3f8 bordetella	967	6	4.4	442	2	Q7S223	Q7s223 neurospora
895	6	4.4	415	2	Q7WES8	Q7wes8 bordetella	968	6	4.4	442	2	Q8X7V2	Q8x7v2 escherichia
896	6	4.4	416	2	Q63H22	Q63h22 bacillus ce	969	6	4.4	444	2	Q937R7	Q937r7 brucella me
897	6	4.4	416	2	Q811Y9	Q81iy9 bacillus ce	970	6	4.4	444	2	Q7MHB0	Q7mhb0 vibrio vuln
898	6	4.4	416	2	Q81VL5	Q81vl5 bacillus an	971	6	4.4	444	2	Q8DCJ8	Q8dcj8 vibrio vuln
899	6	4.4	416	2	Q8DSQ3	Q8dsq3 streptococc	972	6	4.4	444	2	Q8FWL7	Q8fwl7 brucella su
900	6	4.4	417	2	Q6RC07	Q6rc07 mycobacteri	973	6	4.4	444	2	Q9HUR0	Q9hur0 pseudomonas
901	6	4.4	418	2	Q64NZ1	Q64nz1 bacteroides	974	6	4.4	445	2	Q6PCB0	Q6pcb0 homo sapien
902	6	4.4	418	2	Q91GF4	Q91gf4 epiphyas po	975	6	4.4	445	2	Q87YJ5	Q87yj5 pseudomonas
903	6	4.4	418	2	Q90ZA4	Q90za4 anbystoma m	976	6	4.4	446	2	Q8A514	Q8a514 bacteroides
904	6	4.4	419	2	Q84DI2	Q84di2 caulobacter	977	6	4.4	446	2	Q9RSE8	Q9rse8 deinococcus
905	6	4.4	419	2	Q84DI5	Q84di5 caulobacter	978	6	4.4	447	2	Q8SYV3	Q8syv3 drosophila
906	6	4.4	419	2	Q84D18	Q84d18 caulobacter	979	6	4.4	447	2	Q75NB6	Q75nb6 pinctada fu
907	6	4.4	419	2	Q84DJ5	Q84dj5 caulobacter	980	6	4.4	447	2	Q64YV0	Q64yv0 bacteroides


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Qy 61 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREFASDFEVCWCYGNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREFASDFEVCWCYGNRFFRLDLLANEGYL 390

Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405

RESULT 3
Q8WYF7 PRELIMINARY; PRT; 964 AA.
AC Q8WYF7
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE POB1
GN Name=POB1;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu G., Couch F.J.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF213365; AAL36460.1;
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00643; zf-B_box; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00502; BBC; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50144; MATH; 1.
DR PROSITE: PS50119; ZF_BBOX; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
SQ SEQUENCE 964 AA; 107861 MW; 76E5BA4C7901916D CRC64;

Query Match 100.0%; Score 135; DB 2; Length 964;
Best Local Similarity 100.0%; Pred. No. 6e-136;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVVGYLSVPLE 60
Db 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVVGYLSVPLE 330

Qy 61 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREFASDFEVCWCYGNRFFRLDLLANEGYL 120
Db 331 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREFASDFEVCWCYGNRFFRLDLLANEGYL 390

Qy 121 NPQNDTVILRFQVRS 135
Db 391 NPQNDTVILRFQVRS 405

RESULT 4
Q94972 PRELIMINARY; PRT; 979 AA.
AC Q94972
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE KIAA0898 protein (Fragment).
GN Name=KIAA0898;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RL for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL: AB020705; BAA74921.1; -.
DR Genew; HGNC:7523; TRIM37.
DR GO: GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO: GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
DR GO: GO:0016567; P:protein ubiquitination; IEA.
DR InterPro: IPR003649; Bbox_C.
DR InterPro: IPR002083; MATH.
DR InterPro: IPR008974; Traf_like.
DR InterPro: IPR000315; Znf_Bbox.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF00917; MATH; 1.
DR Pfam: PF00643; zf-B_box; 1.
DR PRINTS: PR01406; BBOXZNFINGER.
DR SMART: SM00502; BBC; 1.
DR SMART: SM00336; BBOX; 1.
DR SMART: SM00061; MATH; 1.
DR SMART: SM00184; RING; 1.
DR PROSITE: PS50144; MATH; 1.
DR PROSITE: PS50119; ZF_BBOX; 1.
DR PROSITE: PS50089; ZF_RING_2; 1.
FT NON TER 1
SQ SEQUENCE 979 AA; 109607 MW; D9958FE2EA23EEFD CRC64;

Query Match 100.0%; Score 135; DB 2; Length 979;
Best Local Similarity 100.0%; Pred. No. 6.1e-136;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVVGYLSVPLE 60
Db 286 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPDGVGVVGYLSVPLE 345

Qy 61 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREFASDFEVCWCYGNRFFRLDLLANEGYL 120
Db 346 LSAGLPETSKYEVYRVMVHQSNDPTKNIIREFASDFEVCWCYGNRFFRLDLLANEGYL 405

Qy 121 NPQNDTVILRFQVRS 135
Db 406 NPQNDTVILRFQVRS 420

RESULT 5
Q8CHC5 PRELIMINARY; PRT; 928 AA.
AC Q8CHC5
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE MKIAA0898 protein (Fragment).
GN Name=MKIAA0898;
OS Mus musculus (Mouse);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Okazaki N., Kikuno R., Ohara R., Inamoto S., Hara Y., Nagase T.,
RA Ohara O., Koga H.;
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RL EMBL: AB093271; BAC41455.1; -.
DR EMBL; AB093271; C:intracellular; IEA.
DR GO: GO:0005622; C:intracellular; IEA.
DR GO: GO:0008270; F:zinc ion binding; IEA.
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DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_Like.
DR InterPro; IPR000315; Znf_Box.
DR Pfam; PF00917; MATH; 1.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
FT NON_TER 1
SQ SEQUENCE 928 AA; 103732 MW; 23CEODAAD85BFDE CRC64;

Query Match 89.6%; Score 121; DB 2; Length 928;
Best Local Similarity 100.0%; Pred. No. 6.7e-121;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVGRGYLSVPLE 60
DB 238 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVGRGYLSVPLE 297

QY 61 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCGWGNRFFRLDLLANEGYL 120
DB 298 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCGWGNRFFRLDLLANEGYL 357

QY 121 N 121
DB 358 N 358

RESULT 6
Q6PCX9 ID Q6PCX9 PRELIMINARY; PRT; 961 AA.
AC Q6PCX9
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tripartite motif protein 37.
GN Name=Trim37;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci F., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
[2]
SEQUENCE FROM N.A.
STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
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RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RA Strausberg R.;
RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC059070; AAH59070.1; -.
DR EMBL; BC058678; AAH58678.1; -.
DR GO; GO:0016015; F:morphogen activity; TAS.
DR InterPro; IPR003649; Bbox_C.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_Like.
DR InterPro; IPR000315; Znf_Box.
DR InterPro; IPR001841; Znf_Ring.
DR Pfam; PF00643; zf-B_box; 1.
DR PRINTS; PR01406; BBOXZNFINGER.
DR SMART; SM00502; BBC; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50144; MATH; 1.
DR PROSITE; PS50119; ZF_BBOX; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
SQ SEQUENCE 961 AA; 107659 MW; 85629CBFE0A1D6EA CRC64;

Query Match 89.6%; Score 121; DB 2; Length 961;
Best Local Similarity 100.0%; Pred. No. 6.9e-121;
Matches 121; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVGRGYLSVPLE 60
DB 271 ELVPSYDSATFVLENFSTLRQADPVYSPPLQVSGLCWRLKVPYDGVGVGRGYLSVPLE 330

QY 61 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCGWGNRFFRLDLLANEGYL 120
DB 331 LSAGLPETSKYEVYRVMVHQSCNDPTKNI IREFASDFEGVCGWGNRFFRLDLLANEGYL 390

QY 121 N 121
DB 391 N 391

RESULT 7
Q95LW3 ID Q95LW3 PRELIMINARY; PRT; 721 AA.
AC Q95LW3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Osada N., Hida M., Kusuda J., Tanuma R., Hirata M., Suto Y., Hirai M.,
RA Terao K., Sugano S., Hashimoto K.;
RT "Cynomolgus monkey testicular cDNAs for discovery of novel human genes
RT in the human genome sequence.";
RL BMC Genomics 3:36-36 (2002).
DR EMBL; AB071078; BAB64471.1; -.
DR GO; GO:0000151; C:ubiquitin ligase complex; IEA.
DR GO; GO:0004842; F:ubiquitin-protein ligase activity; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR GO; GO:0016567; P:protein ubiquitination; IEA.
DR InterPro; IPR008974; Traf_Like.
DR InterPro; IPR001841; Znf_Ring.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Hypothetical protein_
SQ SEQUENCE 721 AA; 80131 MW; 203E974760F866E9 CRC64;
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Query Match          47.4%; Score 64; DB 2; Length 721;
Best Local Similarity 100.0%; Pred. No. 1.2e-59;
Matches 64; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 EYRVMVHQSNDPTKNIIRFASDFEVEGECWGNRRFRLLDLANEGYLNFPQNDTVILRF 131
    |||||
Db 100 EYRVMVHQSNDPTKNIIRFASDFEVEGECWGNRRFRLLDLANEGYLNFPQNDTVILRF 159

Qy 132 QVRS 135
    ||||
Db 160 QVRS 163

RESULT 8
G101_HUMAN
ID G101_HUMAN STANDARD; PRT; 508 AA.
AC Q96P66; Q8NG93;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Probable G protein-coupled receptor GPR101.
GN Name=GPR101;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21458557; PubMed=11574155; DOI=10.1016/S0378-1119(01)00651-5;
RA Lee D.K., Nguyen T., Lynch K.R., Cheng R., Vanti W.B., Arkhitko O.,
RA Lewis T., Evans J.F., George S.R., O'Dowd B.F.;
RT "Discovery and mapping of ten novel G protein-coupled receptor
RT genes.";
RL Gene 275:83-91 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040266; PubMed=12044878; DOI=10.1016/S0014-5793(02)02775-8;
RA Takeda S., Kadowaki S., Haga T., Takaesu H., Mitaku S.;
RT "Identification of G protein-coupled receptor genes from the human
RT genome sequence.";
RL FEBS Lett. 520:97-101 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Suwa M., Sato T., Okouchi I., Arita M., Putami K., Matsumoto S.,
RA Tsutsumi S., Aburatani H., Asai K., Akiyama Y.;
RT "Genome-wide discovery and analysis of human seven transmembrane helix
RT receptor genes.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF411115; AAL26486.1; --
CC EMBL; AB083588; BAB89301.1; --
CC EMBL; AB065937; BAC06152.1; ALT_INIT.
CC Genew; HGNC:14963; GPR101.
CC MIM; 300393; --
CC InterPro; IPR000276; GPCR_Rhodpsn.
CC Pfam; PF00001; 7tm_1; 1.
CC PRINTS; PR00237; GPCRHHODOPSN.
CC PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
CC PROSITE; PS0262; G_PROTEIN_RECEP_F1_2; 1.
CC G-protein coupled receptor; Glycoprotein; Transmembrane.
CC DOMAIN 1 35 Extracellular (Potential).
FT
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TRANSMEM 36 56 1 (Potential).
DOMAIN 57 68 Cytoplasmic (Potential).
TRANSMEM 59 89 2 (Potential).
DOMAIN 90 106 Extracellular (Potential).
TRANSMEM 107 127 3 (Potential).
DOMAIN 128 149 Cytoplasmic (Potential).
TRANSMEM 150 170 4 (Potential).
DOMAIN 171 196 Extracellular (Potential).
TRANSMEM 197 217 5 (Potential).
DOMAIN 218 399 Cytoplasmic (Potential).
TRANSMEM 400 420 6 (Potential).
DOMAIN 421 433 Extracellular (Potential).
TRANSMEM 434 454 7 (Potential).
DOMAIN 455 508 Cytoplasmic (Potential).
DISULFID 104 182 By similarity.
CARBOHYD 7 N-linked (GlcNAc...) (Potential).
CARBOHYD 13 N-linked (GlcNAc...) (Potential).
SQ SEQUENCE 508 AA; 56716 MW; E20A409F65C95B85 CRC64;

Query Match          6.7%; Score 9; DB 1; Length 508;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 VPSYDSATF 11
    |||||
Db 499 VPSYDSATF 507

RESULT 9
O34947
ID O34947 PRELIMINARY; PRT; 210 AA.
AC O34947; O79659;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Yoaz.
GN Name=Yoaz; OrderedLocusNames=BSU18790;
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RA Lapidus A., Galleron N., Sorokin A., Ehrlich D.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377; DOI=10.1038/36786;
RA Kunst P., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.-D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Coffeau A., Golightly E.J., Grandi G.,
RA Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.K., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M.,
RA Jones L.-M., Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M.,
RA Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S.,
RA Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J.,
RA Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Maue C.,
RA Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S.,
RA Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B.,
RA Park S.H., Parro T.M., Portetelle D., Porwollik S.,
RA Prescott A.M., Pressecan E., Pujic P., Purnelle B., Rapoport G.,
RA Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B.,
RA Rose M., Sadaie Y., Sato T., Scanlan E., Schleich S., Schroter R.,
RA Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Serro P.,
RA Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H.,
RA Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P.,
RA Tognoni A., Tosato V., Uchiyama S., Vandenberg M., Vannier F.,
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RA Vassarotti A., Viari A., Wambutt R., Wedler E., Wedler H.,
RA Weitzenecker T., Winters P., Wipat A., Yamamoto H., Yamane K.,
RA Yaumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E.,
RA Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
DR EMBL; AF027868; AAB84456.1; -.
DR EMBL; Z99114; CAB13771.1; -.
DR PIR; A69898; A69898.
DR InterPro; IPR002818; ThiJ/Pfpi.
DR Pfam; PF01965; DJ_1_Pfpi; 1.
KW Complete proteome.
SQ SEQUENCE 210 AA; 23420 MW; 19A8BA915AAEF745 CRC64;

Query Match 5.9%; Score 8; DB 2; Length 210;
Best Local Similarity 100.0%; Pred. No. 7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 114 LANEGYLN 121
Db 116 LANEGYLN 123
|||||

RESULT 10
Q65003 PRELIMINARY; PRT; 286 AA.
ID Q65003
AC Q65003;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Putative cell-to-cell movement protein.
OS Apple mosaic virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarvirus.
OX NCBI_TaxID=12319;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95374352; PubMed=7646355;
RA Shiel P.J., Alrefai R.H., Domier L.L., Korban S.S., Berger P.H.;
RT "The complete nucleotide sequence of apple mosaic virus RNA-3.";
RA Arch. Virol. 140:1247-1256(1995).
DR EMBL; U15608; AAA86960.1; -.
DR InterPro; IPR002538; Bromo_MP.
DR Pfam; PF01573; Bromo_MP; 1.
SQ SEQUENCE 286 AA; 32409 MW; D2A4493315A882C1 CRC64;

Query Match 5.9%; Score 8; DB 2; Length 286;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 95 SDFEVEGC 102
Db 10 SDFEVEGC 17
|||||

RESULT 11
Q63CU1 PRELIMINARY; PRT; 423 AA.
ID Q63CU1
AC Q63CU1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase/deaminase family protein.
GN ORFNames=BTZK1681;
OS Bacillus cereus ZK.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=288681;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZK;
RA Bretttin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,

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RA Richardson P., Rubin E., Tice H.;
RT "Complete genome sequence of Bacillus cereus ZK.";
RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; CP000001; AAU18572.1; -.
KW Hydrolase.
SQ SEQUENCE 423 AA; 46816 MW; BD583BC7F209A87B CRC64;

Query Match 5.9%; Score 8; DB 2; Length 423;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 EFASDFEV 99
Db 27 EFASDFEV 34
|||||

RESULT 12
Q81S14 PRELIMINARY; PRT; 435 AA.
ID Q81S14
AC Q81S14; Q61094; Q6KU68;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Chlorohydrolase family protein.
GN OrderedLocusNames=BAL1865, BAS1729, GBAAL1865;
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1392;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate Porton;
MEDLINE=22608414; PubMed=12721629; DOI=10.1039/nature01586;
RA Read T.D., Petersen S.N., Tourasse N.J., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.L.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.B., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.B., Niernan W.C.,
RA Hazen A., Cline R.T., Redmond C., Thwaite J.E., White O.,
RA Salzberg S.L., Thomson B., Friedlander A.M., Koshler T.M.,
RA Hanna P.C., Kolstoe A.-B., Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=Ames / isolate 0581;
RA Ravel J., Rasko D.A., Shumway M.P., Jiang L., Cer R.Z., Federova N.B.,
RA Wilson M., Stanley S., Decker S., Read T.D., Salzberg S.L.,
RA Fraser C.M.;
RT "Bacillus anthracis comparative genomics.";
RL Submitted (MAY-2004) to the EMBL/GenBank/DBSJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Steirne;
RA Bretttin T.S., Bruce D., Challacombe J.F., Gilna P., Han C., Hill K.,
RA Hitchcock P., Jackson P., Keim P., Longmire J., Lucas S., Okinaka R.,
RA Richardson P., Rubin E., Tice H.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; AE017030; AAP25768.1; -.
DR EMBL; AE017334; AAT30980.2; -.
DR EMBL; AE017225; AAT54045.1; -.
DR HSSP; Q9X034; 1P1M.
DR TIGR; BAI1865; -.
DR TIGR; GBAAL1865; -.
DR GO; GO:0016787; P:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro_1.
DR InterPro; IPR011059; Metallohydrolase.
DR Pfam; PF01979; Amidohydro_1; 1.
DR ProDom; PD001248; Amidohydro_like; 1.

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KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48143 MW; 2D2989BAA5819B33 CRC64;
Query Match 5.9%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 EFASDFEV 99
DB 39 EFASDFEV 46

RESULT 13
Q6HK87 PRELIMINARY; PRT; 435 AA.
AC Q6HK87;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Chlorohydrolase/deaminase family protein.
GN OrderedLocusNames=BT9727.1707;
OS Bacillus thuringiensis (subsp. konkukian).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=97-27;
RA Bretin T.S.; Bruce D.; Challacombe J.F.; Gilna P.; Han C.; Hill K.;
RA Hichcock P.; Jackson P.; Keim P.; Longmire J.; Lucas S.; Olinaka R.;
RA Richardson P.; Rubin E.; Tice H.;
RT "Complete genome sequence of Bacillus thuringiensis 97-27.";
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE017355; AAT59611.1;
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR InterPro; IPR006680; Amidohydro_1.
DR InterPro; IPR011550; Amidohydro-like.
DR Pfam; PF01979; Metallo_hydrolase.
DR ProDom; PD001248; Amidohydro_1; 1.
KW Complete proteome; Hydrolase.
SQ SEQUENCE 435 AA; 48139 MW; 6BE505358AE3268 CRC64;

Query Match 5.9%; Score 8; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 92 EFASDFEV 99
DB 39 EFASDFEV 46

RESULT 14
Q8E8R3 PRELIMINARY; PRT; 1045 AA.
ID Q8E8R3;
AC Q8E8R3;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Heavy metal efflux pump, CzcA family.
GN OrderedLocusNames=S04598;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA Heidelberg J.F.; Paulsen I.T.; Nelson K.E.; Gaidos E.J.; Nelson W.C.;
RA Read T.D.; Eisen J.A.; Seshadri R.; Ward N.L.; Methe B.A.;
RA Clayton R.A.; Meyer T.; Tsapin A.; Scott J.; Beanan M.J.;
RA Brinkac L.M.; Daugherty S.C.; DeBoy R.T.; Dodson R.J.; Durkin A.S.;
RA Haft D.H.; Kolonay J.F.; Madupu R.; Peterson J.D.; Umayam L.A.

RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
DR EMBL; AE015891; AAN57558.1; -.
DR TIGR; S04598; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008324; P:cation transporter activity; IEA.
DR GO; GO:0006812; P:cation transporter; IEA.
DR InterPro; IPR003439; ABC_transporter.
DR InterPro; IPR001036; Acriflavin_res.
DR Pfam; PF00873; ACR_tran; 1.
DR PRINTS; PR00702; ACRIFLAVINRP.
DR TIGRfams; TIGR00914; 2A0601; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 1045 AA; 114513 MW; 9E99187C3248C984 CRC64;

Query Match 5.9%; Score 8; DB 2; Length 1045;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 60 ELSAGLPE 67
DB 311 ELSAGLPE 318

RESULT 15
Q89T67 PRELIMINARY; PRT; 98 AA.
ID Q89T67;
AC Q89T67;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Bel2183 protein.
GN OrderedLocusNames=bel2183;
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Idesawa K., Iriguchi M., Kawashima K.,
RA Kohara M., Matsumoto M., Shimo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
RT Bradyrhizobium japonicum USDA110.";
RL DNA Res. 9:189-197(2002).
DR EMBL; AP005942; BAC47448.1; -.
KW Complete proteome.
SQ SEQUENCE 98 AA; 10886 MW; 90279D1E01E99AD5 CRC64;

Query Match 5.2%; Score 7; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 NDTVILR 130
DB 39 NDTVILR 45

Search completed: July 20, 2005, 20:52:18
Job time : 90.75 secs

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OM protein - protein search, using sw model

Run on: July 20, 2005, 20:37:15 ; Search time 85.8 Seconds
(without alignments)
787.814 Million cell updates/sec

Title: US-09-706-325-24

Perfect score: 132

Sequence: 1 SYNWTTNNFSCREMGVEI.....EANGLLPDDKLTLPCEVSVV 132

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	132	100.0	373	2 Q76LV9	Q76LV9 mus musculus
2	132	100.0	374	1 SPOP_HUMAN	Q43791 homo sapien
3	132	100.0	374	1 SPOP_MOUSE	Q8ZWE8 mus musculus
4	132	100.0	374	2 Q8P8B3	Q8P8B3 xenopus tro
5	132	100.0	374	2 Q7T330	Q7T330 brachydanio
6	132	100.0	374	2 Q7ZX06	Q7ZX06 xenopus lae
7	132	100.0	425	2 Q9DB22	Q9DB22 mus musculus
8	53	40.2	391	2 Q9HAB2	Q9HAB2 homo sapien
9	53	40.2	392	2 Q8IQ16	Q8IQ16 homo sapien
10	40	30.3	374	2 Q8MRB4	Q8MRB4 drosophila
11	40	30.3	401	2 Q7PGC0	Q7PGC0 anopheles g
12	40	30.3	403	2 Q8ING4	Q8ING4 drosophila
13	40	30.3	406	2 Q7KSK6	Q7KSK6 drosophila
14	40	30.3	451	1 YNV5_CAEEL	P34568 caenorhabdi
15	40	30.3	695	2 Q7PRD7	Q7PRD7 anopheles g
16	24	18.2	392	2 Q6GR09	Q6GR09 xenopus lae
17	9	6.8	364	2 Q717B2	Q717B2 mus musculus
18	9	6.8	365	2 Q717B4	Q717B4 mus musculus
19	9	6.8	417	2 Q22006	Q22006 bacterioph
20	8	6.1	225	2 Q84ZC8	Q84ZC8 oryza sativ
21	8	6.1	346	2 Q752C0	Q752C0 ashbya goss
22	8	6.1	380	1 HYD1_BRAJA	Q9ANP1 bradyrhizob
23	8	6.1	496	2 Q7RYV4	Q7RYV4 neurospora
24	7	5.3	46	2 Q33589	Q33589 staphylococ
25	7	5.3	46	2 Q7A0E0	Q7A0E0 staphylococ
26	7	5.3	46	2 Q6G7S0	Q6G7S0 staphylococ
27	7	5.3	46	2 Q6GF35	Q6GF35 staphylococ
28	7	5.3	60	2 Q83X46	Q83X46 streptomyce
29	7	5.3	67	2 Q7RU09	Q7RU09 homo sapien
30	7	5.3	88	2 Q8VB68	Q8VB68 white spot
31	7	5.3	91	2 Q7P610	Q7P610 fusobacteri

32	7	5.3	91	2 Q8REL7	Q8REL7 fusobacteri
33	7	5.3	108	2 Q6CUQ4	Q6CUQ4 kluveromyc
34	7	5.3	108	2 Q707Z2	Q707Z2 kluveromyc
35	7	5.3	116	2 Q7X4T0	Q7X4T0 peanut wite
36	7	5.3	136	1 FLIS_ECOLI	P26608 escherichia
37	7	5.3	136	2 Q9FKL7	Q9FKL7 arabidopsis
38	7	5.3	136	2 Q7AD05	Q7AD05 escherichia
39	7	5.3	136	2 Q8XBB7	Q8XBB7 escherichia
40	7	5.3	136	2 Q8FGM0	Q8FGM0 escherichia
41	7	5.3	136	2 Q83R42	Q83R42 shigella fl
42	7	5.3	143	2 Q58831	Q58831 pyrococcus
43	7	5.3	143	2 Q9KOK7	Q9KOK7 vibrio chol
44	7	5.3	156	2 Q8P5Z1	Q8P5Z1 xanthomonas
45	7	5.3	160	2 Q9AVC4	Q9AVC4 xanthomonas
46	7	5.3	172	2 Q8PH48	Q8PH48 xanthomonas
47	7	5.3	187	1 PTH_CHLTE	Q8KD05 chlorobium
48	7	5.3	191	2 Q6FJS6	Q6FJS6 candida gla
49	7	5.3	194	1 GRPE_LACAC	Q84B05 lactobacill
50	7	5.3	197	2 Q9CK36	Q9CK36 pasteurella
51	7	5.3	204	2 Q6LKF0	Q6LKF0 photobacter
52	7	5.3	205	2 Q8RYM7	Q8RYM7 oryza sativ
53	7	5.3	207	2 Q7VXS4	Q7VXS4 bordetella
54	7	5.3	207	2 Q7W6Z7	Q7W6Z7 bordetella
55	7	5.3	207	2 Q7W1V7	Q7W1V7 bordetella
56	7	5.3	213	2 Q8N3C9	Q8N3C9 homo sapien
57	7	5.3	217	2 Q97AQ7	Q97AQ7 thermoplas
58	7	5.3	218	2 Q8C136	Q8C136 mus musculu
59	7	5.3	220	2 Q830M2	Q830M2 enterococcu
60	7	5.3	224	2 Q8C1J8	Q8C1J8 mus musculu
61	7	5.3	224	2 Q9QXH5	Q9QXH5 mus musculu
62	7	5.3	226	2 Q96B00	Q96B00 homo sapien
63	7	5.3	227	2 Q8NHE3	Q8NHE3 homo sapien
64	7	5.3	227	2 Q8TEL0	Q8TEL0 homo sapien
65	7	5.3	231	2 Q9HM62	Q9HM62 thermoplas
66	7	5.3	241	1 GTOI_RAT	Q23339 rattus norv
67	7	5.3	241	2 Q6AXR6	Q6AXR6 rattus norv
68	7	5.3	259	2 Q6T8C8	Q6T8C8 helianthus
69	7	5.3	266	2 Q9DHR7	Q9DHR7 yaba-like d
70	7	5.3	296	1 KHSE_LACLA	Q9CGD7 lactococcus
71	7	5.3	296	1 KHSE_LACLC	P52991 lactococcus
72	7	5.3	298	1 Y5G0_ENCCU	Q8TJ22 encephalito
73	7	5.3	298	2 Q8FMZ0	Q8FMZ0 corynebacte
74	7	5.3	299	2 Q96603	Q96603 plodia inte
75	7	5.3	299	2 Q8GXS4	Q8GXS4 arabidopsis
76	7	5.3	302	2 Q97RX7	Q97RX7 streptococc
77	7	5.3	302	2 Q8FTU2	Q8FTU2 corynebacte
78	7	5.3	304	1 YBBI_BACSU	Q45582 bacillus su
79	7	5.3	310	2 Q9HVV1	Q9HVV1 pseudomonas
80	7	5.3	311	2 Q97ZS5	Q97ZS5 sulfolobus
81	7	5.3	314	2 Q8SUP1	Q8SUP1 encephalito
82	7	5.3	317	2 Q921J9	Q921J9 mus musculu
83	7	5.3	325	2 Q9M212	Q9M212 arabidopsis
84	7	5.3	331	1 RNZ_DEIRA	Q9RXP0 deinococcus
85	7	5.3	340	1 Y100_ARCFU	Q28474 archaeoglob
86	7	5.3	343	2 Q8G9H3	Q8G9H3 nitrosospi
87	7	5.3	345	2 Q8KNY8	Q8KNY8 helicobacte
88	7	5.3	346	2 Q7SLB3	Q7SLB3 neurospora
89	7	5.3	353	2 Q8Z0V7	Q8Z0V7 oryza sativ
90	7	5.3	353	2 Q8C8Y5	Q8C8Y5 mus musculu
91	7	5.3	359	2 Q744A7	Q744A7 mycobacteri
92	7	5.3	361	2 Q8V139	Q8V139 mus musculu
93	7	5.3	365	2 Q717B3	Q717B3 mus musculu
94	7	5.3	365	2 Q71G58	Q71G58 mus musculu
95	7	5.3	365	2 Q8BZV7	Q8BZV7 mus musculu
96	7	5.3	370	2 Q6YCH2	Q6YCH2 mus musculu
97	7	5.3	389	2 Q6R2D1	Q6R2D1 escherichia
98	7	5.3	401	2 Q9SUG5	Q9SUG5 arabidopsis
99	7	5.3	421	1 FXJ1_HUMAN	Q92949 homo sapien
100	7	5.3	421	1 FAXJ1_MOUSE	Q61660 mus musculu
101	7	5.3	421	1 FAXJ1_RAT	Q63247 rattus norv
102	7	5.3	421	2 Q64Q08	Q64Q08 mus musculu
103	7	5.3	440	2 Q73HT1	Q73HT1 wolbachia p
104	7	5.3	441	2 Q9SLB4	Q9SLB4 arabidopsis

105	7	5.3	450	2	Q6LFR8	Q6lfr8 photobacter
106	7	5.3	459	2	Q9K440	Q9k440 streptomyce
107	7	5.3	461	2	Q8FL23	Q8fl23 corynebacte
108	7	5.3	470	2	Q6DVF9	Q6dvf9 podura aqua
109	7	5.3	485	2	Q6QPL8	Q6qpl8 suaeda sald
110	7	5.3	506	2	Q9ACV6	Q9acv6 streptomyce
111	7	5.3	518	2	Q9KHA8	Q9kha8 synecococc
112	7	5.3	518	2	Q9JUA7	Q9jja7 mus musculu
113	7	5.3	520	2	Q96S94	Q96s94 homo sapien
114	7	5.3	563	1	Y963_METJA	Q58373 methanococc
115	7	5.3	567	1	PGTA_HUMAN	Q92696 homo sapien
116	7	5.3	567	1	PGTA_MOUSE	Q91hk4 mus musculu
117	7	5.3	567	1	PGTA_RAT	Q98602 rattus norv
118	7	5.3	567	2	Q8FHF7	Q6fnf7 homo sapien
119	7	5.3	569	2	Q6AN94	Q6an94 desulfotale
120	7	5.3	579	2	Q8BKT3	Q8bkt3 mus musculu
121	7	5.3	644	2	Q43994	Q43994 leishmania
122	7	5.3	644	2	Q8MNY9	Q8mny9 leishmania
123	7	5.3	644	2	Q70W26	Q70w26 leishmania
124	7	5.3	650	2	Q52870	Q52870 rhizobium l
125	7	5.3	657	1	GP63_LEITPR	Q8mnz1 leishmania
126	7	5.3	657	2	Q70W25	Q70w25 leishmania
127	7	5.3	660	2	Q69710	Q69710 mycobacteri
128	7	5.3	660	2	Q7TUTO	Q7tvt0 mycobacteri
129	7	5.3	665	2	Q8BZP4	Q8bzp4 lactobacill
130	7	5.3	678	2	Q8BU31	Q8bu31 debaryomyce
131	7	5.3	684	2	Q8DQP2	Q8dqp2 streptococc
132	7	5.3	733	2	Q7QTS8	Q7qts8 giardia lam
133	7	5.3	745	1	COPB_ENTHR	P05425 enterococcu
134	7	5.3	748	2	Q75JRO	Q75jr0 dictyosteli
135	7	5.3	773	2	Q9IMP3	Q9imp3 influenza c
136	7	5.3	774	1	RRP3_INCBE	P21770 influenza c
137	7	5.3	774	1	RRP3_INCUJ	P13877 influenza c
138	7	5.3	774	2	Q617C4	Q617c4 influenza c
139	7	5.3	774	2	Q82668	Q82668 influenza c
140	7	5.3	801	2	Q6WB34	Q6wb34 alcaligenes
141	7	5.3	817	2	Q73619	P73619 synecocyst
142	7	5.3	844	2	Q9LE38	Q9le38 arabidopsis
143	7	5.3	860	2	Q75BHV9	Q75bv9 ashbya goos
144	7	5.3	868	2	Q7NF67	Q7nf67 gloebacter
145	7	5.3	1009	2	Q6P762	Q6p762 rattus norv
146	7	5.3	1013	1	M2B1_MOUSE	Q09159 mus musculu
147	7	5.3	1066	2	Q7XE90	Q7xe90 oryza sativ
148	7	5.3	1101	2	Q8CPW9	Q8cpw9 kluyveromyc
149	7	5.3	1122	2	Q43945	Q43945 leishmania
150	7	5.3	1293	2	Q9AXD6	Q9axd6 zea mays (m
151	7	5.3	2160	2	O17709	O17709 caenorhabdi
152	7	5.3	2248	2	Q7R5C1	Q7r5c1 giardia lam
153	7	5.3	2397	2	Q7SF97	Q7sf97 neurospora
154	7	5.3	3351	2	Q94907	Q94907 drosophila
155	7	5.3	3351	2	Q9V496	Q9v496 drosophila
156	6	4.5	20	2	Q9QVF9	Q9qvf9 rattus ep.
157	6	4.5	28	2	Q8K1D1	Q8k1d1 mus musculu
158	6	4.5	29	2	Q6EKK8	Q6ekt8 versinia pe
159	6	4.5	40	2	Q6EKU1	Q6ekul versinia pe
160	6	4.5	47	2	Q8FFI2	Q8ffl2 escherichia
161	6	4.5	50	2	Q6GZU6	Q6gzu6 frog virus
162	6	4.5	52	2	Q8ISR4	Q8isr4 spodoptera
163	6	4.5	53	2	Q8VKJ8	Q8vkj8 mycobacteri
164	6	4.5	55	2	Q7MI53	Q7mi53 vibrio vuln
165	6	4.5	56	2	Q9XHG5	Q9xhg5 arabidopsis
166	6	4.5	57	2	Q8CYA4	Q8cy4 streptococc
167	6	4.5	59	2	Q9WPH3	Q9wph3 equid herpe
168	6	4.5	60	2	Q8KEJ9	Q8kej9 chlorobium
169	6	4.5	60	2	Q96744	Q96744 feline herp
170	6	4.5	60	2	Q77VU7	Q77vu7 feline herp
171	6	4.5	60	2	Q77VU8	Q77vu8 feline herp
172	6	4.5	60	2	Q77VU9	Q77vu9 feline herp
173	6	4.5	60	2	Q77VV0	Q77vv0 feline herp
174	6	4.5	65	2	P87439	P87439 lepidodacty
175	6	4.5	65	2	P87440	P87440 lepidodacty
176	6	4.5	65	2	P87443	P87443 lepidodacty
177	6	4.5	65	2	P87449	P87449 lepidodacty

178	6	4.5	65	2	P87450	P87450 lepidodacty
179	6	4.5	65	2	P87451	P87451 lepidodacty
180	6	4.5	65	2	P87454	P87454 lepidodacty
181	6	4.5	65	2	P87455	P87455 lepidodacty
182	6	4.5	66	2	Q63AW0	Q63aw0 bacillus ce
183	6	4.5	67	2	Q73993	Q73993 pyrococcus
184	6	4.5	71	2	Q8VB36	Q8vb36 white spot
185	6	4.5	74	2	Q64Q17	Q64q17 bacteroides
186	6	4.5	76	1	RCRO_BPHKO	P18679 bacterioph
187	6	4.5	76	2	Q8WS66	Q8ws66 glossina mo
188	6	4.5	76	2	Q9PEQ8	Q9peq8 xylella fas
189	6	4.5	77	2	Q21983	Q21983 streptococc
190	6	4.5	80	2	Q74FL0	Q74fl0 geobacter s
191	6	4.5	81	2	Q24497	Q24497 drosophila
192	6	4.5	81	2	Q6MTN0	Q6mnt0 mycoplasma
193	6	4.5	82	2	Q6BQX0	Q6bqx0 debaryomyce
194	6	4.5	82	2	Q684N6	Q684n6 lactobacill
195	6	4.5	82	2	Q8D8S4	Q8d8s4 vibrio vuln
196	6	4.5	83	2	Q74003	Q74003 pyrococcus
197	6	4.5	83	2	Q6QXP5	Q6qxf5 agrotis seg
198	6	4.5	84	2	Q6CSM8	Q6csm8 yarrowia li
199	6	4.5	85	2	Q6G012	Q6g012 bartonella
200	6	4.5	86	1	SCRE_ARATH	P82633 arabidopsis
201	6	4.5	86	2	Q84IM3	Q84im3 clostridium
202	6	4.5	88	1	S61B_KLULA	Q8j2p4 kluyveromyc
203	6	4.5	88	2	Q6AM77	Q6am77 desulfotale
204	6	4.5	90	2	Q75BN7	Q75bn7 ashbya goos
205	6	4.5	90	2	Q6U6G1	Q6u6g1 human herpe
206	6	4.5	91	2	Q9BSG3	Q9bsg3 homo sapien
207	6	4.5	91	2	Q9YMG6	Q9ymg6 lymantria d
208	6	4.5	92	1	RR19_CHAGL	Q8m98 chaetosphae
209	6	4.5	92	1	RS19_THET2	P62660 thermus the
210	6	4.5	92	1	RS19_THETH	P80381 thermus the
211	6	4.5	92	2	Q7S719	Q7s719 neurospora
212	6	4.5	92	2	Q49587	Q49587 mycoplasma
213	6	4.5	93	2	Q9KL08	Q9kl08 vibrio chol
214	6	4.5	93	2	Q95334	Q95334 homo sapien
215	6	4.5	93	2	Q862Y0	Q862y0 bos taurus
216	6	4.5	97	2	Q6D021	Q6d021 erwinia car
217	6	4.5	98	2	Q647N3	Q647n3 uncultured
218	6	4.5	98	2	Q63589	Q63589 florometra
219	6	4.5	99	2	Q65862	Q6b62 hyaloperono
220	6	4.5	101	2	Q974Z5	Q974z5 sulfolobus
221	6	4.5	101	2	Q7N099	Q7n099 photorhabdu
222	6	4.5	101	2	Q81B80	Q81b80 bacillus ce
223	6	4.5	102	2	Q7R334	Q7r334 giardia lam
224	6	4.5	104	2	Q93V87	Q93v87 oryza sativ
225	6	4.5	106	2	Q9XVJ8	Q9xvj8 caenorhabdi
226	6	4.5	106	2	Q9KEL2	Q9kel2 bacillus ha
227	6	4.5	107	1	Y240_RICPR	Q9zdt5 rickettsia
228	6	4.5	107	1	Y324_RICCN	Q92ilu6 rickettsia
229	6	4.5	107	2	Q7PB62	Q7pb62 rickettsia
230	6	4.5	107	2	Q68XC9	Q68xc9 rickettsia
231	6	4.5	108	2	Q8T329	Q8t329 plasmodium
232	6	4.5	108	2	Q8NQW8	Q8nqw8 corynebacte
233	6	4.5	109	2	Q7VCN9	Q7vcn9 prochloroco
234	6	4.5	110	1	RLA2_RHOGU	Q9vcu7 rhodotorula
235	6	4.5	110	2	Q8T5A7	Q8t5a7 plasmodium
236	6	4.5	110	2	Q6TST3	Q6ts3 bacillus sp
237	6	4.5	110	2	Q6TST5	Q6ts5 bacillus sp
238	6	4.5	110	2	Q6TST6	Q6ts6 bacillus sp
239	6	4.5	110	2	Q6TST7	Q6ts7 bacillus sp
240	6	4.5	110	2	Q6TST8	Q6ts8 bacillus sp
241	6	4.5	110	2	Q6TST9	Q6ts9 bacillus sp
242	6	4.5	110	2	Q6TSU0	Q6tsu0 bacillus sp
243	6	4.5	110	2	Q6TSU1	Q6tsu1 bacillus sp
244	6	4.5	110	2	Q6TSU3	Q6tsu3 bacillus sp
245	6	4.5	110	2	Q6TSU5	Q6tsu5 bacillus sp
246	6	4.5	110	2	Q6TSU8	Q6tsu8 bacillus sp
247	6	4.5	110	2	Q6TSV3	Q6tsv3 bacillus sp
248	6	4.5	110	2	Q6TSV4	Q6tsv4 bacillus sp
249	6	4.5	110	2	Q6TSW3	Q6tsw3 bacillus sp
250	6	4.5	110	2	Q6TSW5	Q6tsw5 bacillus sp

251	6	4.5	110	2	Q6TSW9	Q6tsw9 bacillus sp	324	6	4.5	146	2	Q6S8Z5	Q6s8z5 plasmodium
252	6	4.5	110	2	Q6TSX2	Q6tsx2 bacillus sp	325	6	4.5	146	2	Q6S8Z5	Q6s8z5 plasmodium
253	6	4.5	110	2	Q6TSX3	Q6tsx3 bacillus sp	326	6	4.5	147	1	FUR_MYCTU	Q6s8z5 mycobacteri
254	6	4.5	110	2	Q6TSX4	Q6tsx4 bacillus sp	327	6	4.5	147	2	Q7REC7	Q7rec7 mycobacteri
255	6	4.5	110	2	Q6TSX7	Q6tsx7 bacillus sp	328	6	4.5	147	2	Q9LALO	Q9lal0 mycobacteri
256	6	4.5	110	2	Q6TSX8	Q6tsx8 bacillus sp	329	6	4.5	147	2	Q64ZR3	Q64zr3 bacteroides
257	6	4.5	110	2	Q6TSX9	Q6tsx9 bacillus sp	330	6	4.5	148	2	Q9EX95	Q9ex95 pseudomonas
258	6	4.5	110	2	Q6TSY7	Q6tsy7 bacillus ce	331	6	4.5	148	2	Q84143	Q84143 chlamydia t
259	6	4.5	110	2	Q6TSZ1	Q6tsz1 bacillus sp	332	6	4.5	148	2	Q7UBER1	Q7ueel rhodopirell
260	6	4.5	110	2	Q6TSZ2	Q6tsz2 bacillus sp	333	6	4.5	150	1	RL10_TOBAC	Q40592 nicotiana t
261	6	4.5	110	2	Q6TSZ3	Q6tsz3 bacillus sp	334	6	4.5	150	2	Q6V5E2	Q6v5e2 olimarabido
262	6	4.5	110	2	Q6DGM0	Q6dgm0 brachydanio	335	6	4.5	152	2	Q9S5X26	Q9s5x26 caenorhabdi
263	6	4.5	111	2	Q9FTX6	Q9ftx6 oryza sativ	336	6	4.5	152	2	Q8VL41	Q8v141 streptococc
264	6	4.5	112	2	Q8W1C9	Q8w1c9 zea mays (m	337	6	4.5	152	2	Q8VVY6	Q8vvv6 streptococc
265	6	4.5	112	2	Q6K8U8	Q6k8u8 oryza sativ	338	6	4.5	152	2	Q8VVY7	Q8vvv7 streptococc
266	6	4.5	112	2	Q8ATF4	Q8atf4 castanea sa	339	6	4.5	152	2	Q8VVY8	Q8vvv8 streptococc
267	6	4.5	112	2	Q9ATW9	Q9atw9 zea mays (m	340	6	4.5	152	2	Q8VVY9	Q8vvv9 streptococc
268	6	4.5	112	2	Q98M13	Q98m13 rhizobium l	341	6	4.5	152	2	Q8VVZ0	Q8vvz0 streptococc
269	6	4.5	113	2	Q6B8P1	Q6b8p1 gracilaria	342	6	4.5	152	2	Q8XTH3	Q8xth3 raietonia s
270	6	4.5	113	1	S206_HUMAN	P80162 homo sapien	343	6	4.5	153	2	Q82RR6	Q82rr6 streptomyce
271	6	4.5	114	2	Q9RZG3	Q9rzg3 deinococcus	344	6	4.5	154	2	Q8SFW7	Q8sfw7 cacopsylla
272	6	4.5	117	1	RNPA_THEME	Q9x1b4 thermotoga	345	6	4.5	156	1	AP19_YEAST	P35181 saccharomyc
273	6	4.5	118	2	Q64E23	Q64e23 uncultured	346	6	4.5	156	2	Q6FXK8	Q6fxk8 candida gla
274	6	4.5	118	2	Q9YAG7	Q9yag7 aeropyrum p	347	6	4.5	156	2	Q70ZG4	Q70z94 canis famil
275	6	4.5	118	2	Q8ZMQ6	Q8zmq6 salmonella	348	6	4.5	156	2	Q70ZG4	Q70z94 canis famil
276	6	4.5	119	2	Q93VLO	Q93v10 arabidopsis	349	6	4.5	156	2	Q9M2T2	Q9m2t2 arabidopsis
277	6	4.5	120	2	Q58311	Q58311 pyrococcus	350	6	4.5	156	2	Q6S7M3	Q6s7m3 uncultured
278	6	4.5	120	2	Q77196	Q77196 plasmodium	351	6	4.5	156	2	Q8XLL8	Q8xll8 clostridium
279	6	4.5	121	1	ML30_ARATH	P33282 arabidopsis	352	6	4.5	157	1	VHCB_METVO	Q50849 methanococc
280	6	4.5	122	2	Q7SA46	Q7sa46 neurospora	353	6	4.5	157	2	Q8L8T8	Q8l8t8 arabidopsis
281	6	4.5	123	2	Q8ST88	Q8st88 plasmodium	354	6	4.5	157	2	Q9C8Y1	Q9c8y1 arabidopsis
282	6	4.5	124	2	Q8CTW6	Q8ctw6 staphylococ	355	6	4.5	157	2	Q7N3S4	Q7n3s4 photorhabdu
283	6	4.5	128	2	Q95W38	Q95w38 schistocerc	356	6	4.5	158	2	Q91C95	Q91c95 pan rhadino
284	6	4.5	128	2	Q6S8X6	Q6s8x6 plasmodium	357	6	4.5	159	2	Q74N72	Q74ni2 nanoarchaeu
285	6	4.5	128	2	Q9HXC8	Q9hxc8 pseudomonas	358	6	4.5	159	2	Q8RPA7	Q8rpa7 pseudomonas
286	6	4.5	129	1	Q98ML1	P34386 caenorhabdi	359	6	4.5	160	2	Q7XXS2	Q7xxs2 oryza sativ
287	6	4.5	131	2	Q98ML1	Q98ml1 rhizobium l	360	6	4.5	161	2	Q7PMF0	Q7pmf0 anopheles g
288	6	4.5	131	2	Q6MU42	Q6mu42 mycoplasma	361	6	4.5	162	2	Q7TFX4	Q7tfx4 rhesus cyto
289	6	4.5	131	2	Q7VNO4	Q7vnu4 haemophilus	362	6	4.5	165	2	Q75SF2	Q75sf2 drosophila
290	6	4.5	131	2	Q99LW1	Q99lw1 mus musculu	363	6	4.5	165	2	Q7VM67	Q7vm67 haemophilus
291	6	4.5	132	2	Q6LZJ8	Q6lzt8 methanococc	364	6	4.5	166	1	VG17_BPPH2	P33686 bacteriophag
292	6	4.5	132	2	Q9BQX0	Q9bqx0 homo sapien	365	6	4.5	166	2	Q6CPI1	Q6cp11 kluveromyce
293	6	4.5	133	2	Q6ZS21	Q6zst1 homo sapien	366	6	4.5	166	2	Q6WCC1	Q6wcc1 serratia pr
294	6	4.5	133	2	Q6WS74	Q6wst4 perinereis	367	6	4.5	167	2	Q75SH2	Q75sh2 drosophila
295	6	4.5	133	2	Q9U511	Q9u511 manduca sex	368	6	4.5	167	2	Q64XB3	Q64xb3 bacteroides
296	6	4.5	133	2	Q9U513	Q9u513 manduca sex	369	6	4.5	167	2	Q8YX42	Q8yx42 anabaena sp
297	6	4.5	133	2	Q9FHG2	Q9fhg2 arabidopsis	370	6	4.5	167	2	Q98D81	Q98d81 rhizobium l
298	6	4.5	134	2	Q8T589	Q8t589 plasmodium	371	6	4.5	168	1	PLAS_POPNI	P00299 populus nig
299	6	4.5	134	2	Q92NY3	Q92ny3 rhizobium m	372	6	4.5	168	1	PLAT_POPNI	P11970 populus nig
300	6	4.5	135	2	Q6LY91	Q6ly91 methanococc	373	6	4.5	168	2	Q97WD3	Q97wd3 sulfolobus
301	6	4.5	135	2	Q9YBJ8	Q9ybj8 aeropyrum p	374	6	4.5	169	2	Q8UI76	Q8uit6 pyrococcus
302	6	4.5	135	2	Q6S8X7	Q6s8x7 plasmodium	375	6	4.5	169	2	Q6XCE6	Q6xce6 carvus elap
303	6	4.5	135	2	Q8SFW6	Q8sfw6 cacopsylla	376	6	4.5	169	2	Q8RF59	Q8rf59 fusobacteri
304	6	4.5	137	2	Q8LHB2	Q8lhb2 oryza sativ	377	6	4.5	170	2	Q87J70	Q87j70 vibrio para
305	6	4.5	138	2	Q63BE4	Q63be4 bacillus ce	378	6	4.5	171	2	Q7UGP2	Q7ugp2 rhodopirell
306	6	4.5	138	2	Q738D3	Q738d3 bacillus ce	379	6	4.5	171	2	Q69504	Q69504 human herpe
307	6	4.5	138	2	Q6H1S8	Q6his8 bacillus th	380	6	4.5	172	2	Q9XLW7	Q9x1w7 leishmania
308	6	4.5	140	2	Q7Z477	Q7z477 homo sapien	381	6	4.5	172	2	Q6IU31	Q6iu31 escherichia
309	6	4.5	140	2	Q824S1	Q824s1 chlamydophi	382	6	4.5	173	2	Q8WOC7	Q8woc7 oryza sativ
310	6	4.5	140	2	Q8E124	Q8e124 shewanella	383	6	4.5	173	2	Q40650	Q40650 oryza sativ
311	6	4.5	140	2	Q9PJJ1	Q9pj11 chlamydia m	384	6	4.5	174	1	RECR_HABDU	Q30823 haemophilus
312	6	4.5	141	2	Q6S8P8	Q6s8p8 plasmodium	385	6	4.5	174	2	Q7S726	Q7s726 neurospora
313	6	4.5	141	2	Q84554	Q84554 chlamydia t	386	6	4.5	175	2	Q8TM14	Q8tm14 methanosarc
314	6	4.5	142	2	Q8ZT24	Q8zt24 pyrobaculum	387	6	4.5	176	2	Q8TP13	Q8tp13 methanosarc
315	6	4.5	142	2	Q9Z7N3	Q9z7n3 chlamydia p	388	6	4.5	178	2	Q7V6S3	Q7v6s3 prochloroco
316	6	4.5	142	2	Q6D6B6	Q6d6b6 erwinia car	389	6	4.5	178	2	Q9DEQ7	Q9deq7 gallus gall
317	6	4.5	143	2	Q6S8Q0	Q6s8q0 plasmodium	390	6	4.5	180	1	RRF_CHLPN	Q9z7k6 chlamydia p
318	6	4.5	143	2	Q8DS73	Q8ds73 streptococc	391	6	4.5	180	2	Q8ESH2	Q8esh2 streptococc
319	6	4.5	144	2	Q8RYD4	Q8ryd4 ovis aries	392	6	4.5	181	2	Q8E543	Q8e543 streptococc
320	6	4.5	144	2	Q9Z2S8	Q9z2s8 rhizobium m	393	6	4.5	182	2	Q979F9	Q979f9 thermoplasm
321	6	4.5	144	2	Q8BF75	Q8bft5 m mus muscu	394	6	4.5	182	2	Q54202	Q54202 streptomyce
322	6	4.5	145	2	Q711H5	Q711h5 lactobacill	395	6	4.5	183	2	Q8DZS3	Q8dzs3 streptococc
323	6	4.5	146	2	Q6FNC9	Q6fnc9 candida gla	396	6	4.5	184	1	KAD2_ANASP	Q8z0m3 anabaena sp

397	6	4.5	184	2	Q96HR9	Q96hr9 homo sapien	470	6	4.5	214	2	Q66VF0	O66vf0 gekko japon
398	6	4.5	184	2	Q96LMO	Q96lmo homo sapien	471	6	4.5	214	2	Q80IH9	Q80ih9 petromyzon
399	6	4.5	184	2	Q96GH7	Q96gh7 arabidopsis	472	6	4.5	214	2	Q64IS6	Q64is6 xenopus lae
400	6	4.5	185	2	Q96WF6	Q96wf6 lomix hirta	473	6	4.5	215	2	Q7PQZ6	Q7pqz6 anopheles g
401	6	4.5	186	2	Q94SR9	Q94sr9 oryza sativ	474	6	4.5	215	2	Q6KIE5	Q6kie5 mycoplasma
402	6	4.5	186	2	Q68JS7	Q68js7 gopherus po	475	6	4.5	215	2	Q88GV6	Q88gv6 pseudomonas
403	6	4.5	188	2	Q9AW09	Q9aw09 guillardia	476	6	4.5	215	2	Q6VTR3	Q6vt3 choristoneu
404	6	4.5	188	2	Q98DN2	Q98dn2 fusobacteri	477	6	4.5	215	2	Q90YV9	Q90yv9 ictalurus p
405	6	4.5	189	2	Q98S03	Q98s03 arabidopsis	478	6	4.5	215	2	Q6DIQ8	Q6diq8 xenopus tro
406	6	4.5	189	2	Q92CL2	Q92cl2 listeria in	479	6	4.5	215	2	Q7ZV96	Q7zv96 brachydanio
407	6	4.5	190	2	Q63R83	Q63r83 burkholderi	480	6	4.5	215	2	Q7ZXK4	Q7zxk4 xenopus lae
408	6	4.5	190	2	Q65NC7	Q65nc7 bacillus li	481	6	4.5	216	1	SPR2_IPOBA	P14716 ipomeea bat
409	6	4.5	191	1	YK25_YEAST	Q65nc7 saccharomyc	482	6	4.5	216	1	SPR8_IPOBA	P10965 ipomeea bat
410	6	4.5	191	2	Q264F8	Q264f8 schistocerc	483	6	4.5	216	2	Q970W9	Q970w9 sulfolobus
411	6	4.5	191	2	Q6XHV6	Q6xhv6 drosophila	484	6	4.5	216	2	Q6LCG6	Q6lcg6 hydra atten
412	6	4.5	191	2	Q9K3Q0	Q9k3q0 streptomyce	485	6	4.5	216	2	Q86QS5	Q86qs5 brachiosteo
413	6	4.5	192	1	KADA_METJJA	P43409 methanococc	486	6	4.5	216	2	Q70Z95	Q70z95 canis famil
414	6	4.5	193	2	Q9YEL3	Q9yel3 aeropyrum p	487	6	4.5	216	2	Q40091	Q40091 ipomeea bat
415	6	4.5	193	2	Q86LY0	Q86ly0 myxine glut	488	6	4.5	216	2	Q6DV42	Q6dv42 camellia si
416	6	4.5	193	2	Q86LY1	Q86ly1 brachiosteo	489	6	4.5	216	2	Q6DV76	Q6dv76 cardagana ju
417	6	4.5	193	2	Q81WB0	Q81wb0 bacillus an	490	6	4.5	216	2	Q7WAU4	Q7wau4 bordetella
418	6	4.5	195	2	Q97B70	Q97b70 thermoplasma	491	6	4.5	217	2	Q8PV90	Q8pv90 methanosarc
419	6	4.5	198	2	Q69QA7	Q69qa7 oryza sativ	492	6	4.5	217	2	Q83DJ4	Q83dj4 coxiella bu
420	6	4.5	198	2	Q92XJ6	Q92xj6 rhizobium m	493	6	4.5	218	1	R102_ORYSA	P45636 oryza sativ
421	6	4.5	198	2	Q92N06	Q92n06 streptomyce	494	6	4.5	218	1	RL10_DROME	O61231 drosophila
422	6	4.5	199	2	Q94WV1	Q94wv1 mastigoproce	495	6	4.5	218	2	Q6XIN5	Q6xins drosophila
423	6	4.5	201	1	Y802_NEIMA	Q9jvk3 neisseria m	496	6	4.5	219	1	R103_ORYSA	Q96649 oryza sativ
424	6	4.5	201	2	Q8SQA5	Q8sqas bos taurus	497	6	4.5	219	1	RL10_BOMMA	Q96647 bombyx mand
425	6	4.5	201	2	Q8YNG8	Q8ynj8 anabaena sp	498	6	4.5	219	1	RL10_SOLME	P93847 solanum mel
426	6	4.5	202	1	COAT_ELV	P35927 erysimum la	499	6	4.5	219	1	SPR1_IPOBA	P14715 ipomeea bat
427	6	4.5	202	1	Y598_NEIMB	Q9k0j8 neisseria m	500	6	4.5	219	1	SPRA_IPOBA	P10917 ipomeea bat
428	6	4.5	202	2	Q93EK2	Q93ek2 saccharopol	501	6	4.5	219	2	Q6UXZ8	Q6uxz8 homo sapien
429	6	4.5	202	2	Q9RG18	Q9rgi8 bacteroides	502	6	4.5	219	2	Q9SP53	Q9sp53 bombyx mori
430	6	4.5	202	2	Q7N3T9	Q7n3t9 photorhabdu	503	6	4.5	219	2	Q9SPD4	Q9spd4 heliothis v
431	6	4.5	203	1	YL36_YEAST	Q97986 saccharomyc	504	6	4.5	219	2	Q6F451	Q6f451 pluteilla xy
432	6	4.5	204	2	Q8NIX6	Q8nix6 neopospora	505	6	4.5	219	2	Q7PSW8	Q7psw8 anopheles g
433	6	4.5	204	2	Q8HJK8	Q8hjk8 brachidonte	506	6	4.5	219	2	Q8VWX0	Q8vwx0 ipomeea bat
434	6	4.5	204	2	Q8HJK9	Q8hjk9 brachidonte	507	6	4.5	219	2	Q40084	Q40084 ipomeea bat
435	6	4.5	204	2	Q8EMN1	Q8emn1 oceanobacil	508	6	4.5	219	2	Q40085	Q40085 ipomeea bat
436	6	4.5	205	2	Q61IL5	Q61il5 drosophila	509	6	4.5	219	2	Q40092	Q40092 ipomeea bat
437	6	4.5	205	2	Q34560	Q34560 geukensia d	510	6	4.5	219	2	Q9SWG8	Q9swg8 ipomeea bat
438	6	4.5	205	2	Q66676	Q66676 equid herpe	511	6	4.5	219	2	Q9ZSC7	Q9zsc7 ipomeea bat
439	6	4.5	207	2	Q9NX03	Q9nx03 homo sapien	512	6	4.5	219	2	Q7MAJ2	Q7maj2 wolinnella s
440	6	4.5	207	2	Q7X1S5	Q7x1s5 pseudomonas	513	6	4.5	219	2	Q87ES3	Q87es3 xylella fas
441	6	4.5	208	2	Q8A723	Q8a723 bacteroides	514	6	4.5	219	2	Q9PGM0	Q9pgm0 xylella fas
442	6	4.5	208	2	Q8A788	Q8a788 bacteroides	515	6	4.5	219	2	Q810E5	Q810e5 mus musculus
443	6	4.5	210	1	RL10_CHICK	Q80200 gallus gall	516	6	4.5	220	1	RL10_EUPES	Q9m5n7 euphorbia e
444	6	4.5	210	2	Q67A25	Q67a25 thalicttrum	517	6	4.5	220	1	RL10_MAIZE	P45633 zea mays (m
445	6	4.5	210	2	Q62FC9	Q62fc9 burkholderi	518	6	4.5	220	1	RL10_VITRI	Q9epb3 vitis ripar
446	6	4.5	210	2	Q83XL2	Q83xl2 burkholderi	519	6	4.5	220	2	Q05942	Q05942 saccharomyc
447	6	4.5	210	2	Q87DB5	Q87db5 xylella fas	520	6	4.5	220	2	Q93VT9	Q93vt9 arabidopsis
448	6	4.5	210	2	Q9PD54	Q9pd54 xylella fas	521	6	4.5	220	2	Q34213	Q34213 pectobacter
449	6	4.5	211	2	Q9CTD2	Q9ctd2 mus musculus	522	6	4.5	221	1	RL10_ARATH	Q08770 arabidopsis
450	6	4.5	211	2	Q7RQK7	Q7rqk7 plasmodium	523	6	4.5	221	2	Q93W22	Q93w22 arabidopsis
451	6	4.5	211	2	Q9QUL0	Q9qul0 rattus norv	524	6	4.5	221	2	Q6MLJ4	Q6mlu4 bdellovibri
452	6	4.5	211	2	Q9R0S7	Q9r0s7 rattus norv	525	6	4.5	221	2	Q8ETG6	Q8etg6 oceanobacil
453	6	4.5	212	1	RL10_PIG	Q29195 sus scrofa	526	6	4.5	222	2	Q6P7R1	Q6p7r1 rattus norv
454	6	4.5	212	2	Q7PFX12	Q7pxi2 anopheles g	527	6	4.5	223	1	CYPH_NEUCR	P10255 neopospora
455	6	4.5	212	2	Q8R7Q7	Q8r7q7 thermoanaer	528	6	4.5	223	2	Q6JTL6	Q6jtl6 dianema lon
456	6	4.5	213	1	RL10_BOVIN	Q9xsl3 bos taurus	529	6	4.5	223	2	Q8LJX4	Q8ljx4 sorghum bic
457	6	4.5	213	1	RL10_HUMAN	P27635 homo sapien	530	6	4.5	223	2	Q9SDE0	Q9sde0 oryza sativ
458	6	4.5	213	1	RL10_MOUSE	Q8zvw3 mus musculus	531	6	4.5	223	2	Q9WHA5	Q9wha5 human herpe
459	6	4.5	213	1	RL10_RAT	Q8pdv7 rattus norv	532	6	4.5	224	1	R101_ORYSA	P45635 oryza sativ
460	6	4.5	213	2	Q8TDA5	Q8tda5 homo sapien	533	6	4.5	224	2	Q9FUN3	Q9fun3 elaeis guin
461	6	4.5	214	1	1432_SCMA	Q26537 schistosoma	534	6	4.5	224	2	Q9LA99	Q9la99 aeromonas h
462	6	4.5	214	1	RL10_CABEL	Q09533 caenorhabdi	535	6	4.5	224	2	Q6FB64	Q6fb64 acinetobact
463	6	4.5	214	2	Q96L21	Q96l21 homo sapien	536	6	4.5	224	2	Q9Q0B1	Q9qob1 anticarsia
464	6	4.5	214	2	Q6LAG5	Q6lag5 suberites d	537	6	4.5	225	2	Q40129	Q40129 lycopersico
465	6	4.5	214	2	Q9FVN3	Q9fvn3 oryza sativ	538	6	4.5	226	1	PRL_RAT	P01237 rattus norv
466	6	4.5	214	2	Q97HN7	Q97hn7 clostridium	539	6	4.5	226	2	Q6KZZ4	Q6kzz4 picrophilus
467	6	4.5	214	2	Q82315	Q82315 chlamydomophi	540	6	4.5	226	2	Q6MM63	Q6mm63 bdellovibri
468	6	4.5	214	2	Q87ZV3	Q87zv3 pseudomonas	541	6	4.5	226	2	Q7VUM4	Q7vum4 bordetella
469	6	4.5	214	2	Q89EB2	Q89eb2 bradyrhizob	542	6	4.5	226	2	Q7W1Z1	Q7w1z1 bordetella

543	6	4.5	226	2	Q7WQW9	Q7wqw9 bordetella	616	6	4.5	249	2	Q6NZA9	Q6nza9 mus musculus
544	6	4.5	227	2	Q7VH12	Q7vhl2 homo sapien	617	6	4.5	250	1	Y035_METJA	Q50350 methanococc
545	6	4.5	227	2	Q7VHS9	Q7vhs9 helicobacte	618	6	4.5	251	1	Y297_METJA	Q57745 methanococc
546	6	4.5	227	2	Q8G547	Q8g547 bifidobacte	619	6	4.5	251	2	Q9HBM6	Q9hbm6 homo sapien
547	6	4.5	227	2	Q9WH41	Q9wh41 human herpe	620	6	4.5	251	2	Q9Y283	Q9y283 homo sapien
548	6	4.5	228	1	EA5B_BRARE	P79728 brachydanio	621	6	4.5	251	2	Q6LIU99	Q6liu99 drosophila
549	6	4.5	228	1	RL10_PINTA	Q22431 pinus taeda	622	6	4.5	251	2	Q7QP34	Q7qp34 giardia lam
550	6	4.5	228	1	Q6M0F2	Q6m0f2 methanococc	623	6	4.5	252	2	Q80WM6	Q80wm6 mus musculus
551	6	4.5	229	1	MODB_ECOLI	P09834 escherichia	624	6	4.5	253	1	TAF9_RAT	Q62880 rattus norv
552	6	4.5	229	1	Q8ZXF5	Q8zxr5 pyrobaculum	625	6	4.5	253	2	Q6CVM4	Q6cvm4 kluyveromyc
553	6	4.5	229	2	Q8XH21	Q8xh21 salmonella	626	6	4.5	254	2	Q8IXE7	Q8ixe7 homo sapien
554	6	4.5	229	2	Q7CQW7	Q7cq7 salmonella	627	6	4.5	254	2	Q27936	Q27936 fasciola he
555	6	4.5	229	2	Q87HN3	Q87hn3 vibrio para	628	6	4.5	254	2	Q98NV7	Q98nv7 rhizobium l
556	6	4.5	229	2	Q8FJR5	Q8fjr5 escherichia	629	6	4.5	254	2	Q83A76	Q83a76 coxiella bu
557	6	4.5	229	2	Q83SA6	Q83sa6 shigella fl	630	6	4.5	254	2	Q641A8	Q641a8 xenopus lae
558	6	4.5	229	2	Q9WHB1	Q9whb1 human herpe	631	6	4.5	255	2	Q8YX23	Q8yx23 anabaena sp
559	6	4.5	231	1	YE12_YEAST	P39975 saccharomyc	632	6	4.5	255	2	Q8CKN3	Q8ckn3 yersinia pe
560	6	4.5	231	2	Q8B1N5	Q8bin5 saccharomyc	633	6	4.5	257	2	Q8GQA2	Q8gqa2 pseudomonas
561	6	4.5	231	2	Q8YL15	Q8yll5 anabaena sp	634	6	4.5	258	2	Q98S77	Q98s77 guillardia
562	6	4.5	231	2	Q9CY14	Q9cy14 mus musculus	635	6	4.5	259	2	Q7PF71	Q7pf71 anopheles g
563	6	4.5	232	1	RNP3_METMP	P60781 methanococc	636	6	4.5	259	2	Q6UV34	Q6uv34 rattus norv
564	6	4.5	232	1	UBIG_PSRPK	Q88m10 pseudomonas	637	6	4.5	259	2	Q7TP20	Q7tp20 rattus norv
565	6	4.5	232	1	UBIG_PSESM	Q885t9 pseudomonas	638	6	4.5	260	2	Q7MU70	Q7mu70 porphyromon
566	6	4.5	232	2	Q92U16	Q92ut6 rhizobium m	639	6	4.5	261	1	COBS_BACHD	Q9ckn9 bacillus ha
567	6	4.5	232	2	Q97I18	Q97ie8 clostridium	640	6	4.5	261	2	Q66FP2	Q66fp2 yersinia ps
568	6	4.5	233	1	BCLA_HUMAN	Q95999 h b cell ly	641	6	4.5	261	2	Q8ZAQ6	Q8zaq6 yersinia pe
569	6	4.5	233	1	BCLA_RAT	Q95999 h b cell ly	642	6	4.5	261	2	Q9KGC6	Q9kgc6 bacillus ha
570	6	4.5	233	2	Q67NT0	Q67nt0 symbiobacte	643	6	4.5	262	2	Q6CTE9	Q6cte9 kluyveromyc
571	6	4.5	233	2	Q8G6E8	Q8g6e8 bifidobacte	644	6	4.5	262	2	Q9KHD9	Q9khd9 streptomyc
572	6	4.5	233	2	Q928V6	Q928v6 chlamydia p	645	6	4.5	262	2	Q8CJV4	Q8civ4 streptomyc
573	6	4.5	234	2	Q9H6D8	Q9h6d8 homo sapien	646	6	4.5	263	2	Q6XCF0	Q6xcf0 alces alces
574	6	4.5	234	2	Q935Q2	Q935q2 salmonella	647	6	4.5	264	1	TAF9_HUMAN	Q16594 homo sapien
575	6	4.5	235	2	Q8YTO9	Q8yto9 anabaena sp	648	6	4.5	264	1	TAF9_MOUSE	Q8v133 mus musculus
576	6	4.5	236	2	Q62HY4	Q62hy4 burkholderi	649	6	4.5	264	2	Q7PVAB	Q7pva8 anopheles g
577	6	4.5	238	2	Q22135	Q22135 arabidopsis	650	6	4.5	264	2	Q6XCE9	Q6xce9 ovis aries
578	6	4.5	238	2	Q53167	Q53167 rhizobium s	651	6	4.5	265	2	Q6LI99	Q6li99 picrophilus
579	6	4.5	239	1	Y352_METJA	Q57798 methanococc	652	6	4.5	265	2	Q6FY89	Q6fy89 candida gla
580	6	4.5	239	2	Q8A704	Q8a704 bacteroides	653	6	4.5	266	2	Q72PQ3	Q72pq3 leptospira
581	6	4.5	239	2	Q8DMG3	Q8dmg3 synechococc	654	6	4.5	266	2	Q8F6K0	Q8f6k0 leptospira
582	6	4.5	240	2	Q73KH0	Q73kh0 treponema d	655	6	4.5	267	2	Q70K03	Q70k03 bacillus am
583	6	4.5	241	2	Q7PK32	Q7pke2 anopheles g	656	6	4.5	268	2	Q650W0	Q650w0 oryza sativ
584	6	4.5	241	2	Q7QLB6	Q7qlb6 anopheles g	657	6	4.5	268	2	Q98M34	Q98m34 rhizobium l
585	6	4.5	241	2	Q7A0U4	Q7aou4 staphylococ	658	6	4.5	269	1	6PGL_CABEL	Q18229 caenorhabdi
586	6	4.5	241	2	Q7A2R6	Q7a2r6 staphylococ	659	6	4.5	269	2	Q9ZUA7	Q9zua7 arabidopsis
587	6	4.5	241	2	Q7A5H6	Q7a5h6 staphylococ	660	6	4.5	270	1	FLHO_BACSU	P39752 bacillus su
588	6	4.5	241	2	Q8CP56	Q8cp56 staphylococ	661	6	4.5	270	2	Q8L9Q4	Q8l9q4 arabidopsis
589	6	4.5	241	2	Q8DL16	Q8dl16 synechococc	662	6	4.5	271	2	Q9SKU8	Q9skus arabidopsis
590	6	4.5	241	2	Q8DLT9	Q8dl19 synechococc	663	6	4.5	272	2	Q9F7L9	Q9ftl9 gamma-prote
591	6	4.5	241	2	Q9L524	Q9l524 staphylococ	664	6	4.5	273	2	Q7VTP1	Q7vtp1 bordetella
592	6	4.5	241	2	Q62076	Q62076 mus musculus	665	6	4.5	273	2	Q7W150	Q7w150 bordetella
593	6	4.5	242	2	Q7Q617	Q7q617 anopheles g	666	6	4.5	273	2	Q7WNU0	Q7wnu0 bordetella
594	6	4.5	242	2	Q7P642	Q7p642 fusobacteri	667	6	4.5	273	2	Q6D636	Q6d636 erwinia car
595	6	4.5	242	2	Q8RGQ1	Q8rgq1 fusobacteri	668	6	4.5	274	2	Q8VZ41	Q8vz41 arabidopsis
596	6	4.5	242	2	Q97N70	Q97n70 streptococc	669	6	4.5	275	2	Q88LI1	Q88li1 pseudomonas
597	6	4.5	242	2	Q8DMZ8	Q8dmz8 streptococc	670	6	4.5	276	2	Q9IC27	Q9ic27 human herpe
598	6	4.5	243	2	Q7NFY9	Q7nfy9 gloeobacter	671	6	4.5	277	2	Q6CIN5	Q6cin5 yarrowia li
599	6	4.5	243	2	Q8DMH9	Q8dm9 synechococc	672	6	4.5	278	1	URED_ECOLI	Q03285 escherichia
600	6	4.5	244	1	TP1S_DEIRA	Q8rups deinococcus	673	6	4.5	279	1	EFTS_BORBU	Q51148 borrelia bu
601	6	4.5	244	2	Q8FDL4	Q8fdl4 escherichia	674	6	4.5	279	1	Y144_MYCGE	P47390 mycoplasma
602	6	4.5	245	2	Q9VPM1	Q9vpm1 drosophila	675	6	4.5	279	2	Q93LC0	Q93lc0 salmonella
603	6	4.5	245	2	Q6YK36	Q6yk36 bacillus su	676	6	4.5	279	2	Q662P0	Q662p0 borrelia ga
604	6	4.5	245	2	Q97HU5	Q97hj5 clostridium	677	6	4.5	279	2	Q9CNN0	Q9cnn0 pasteurella
605	6	4.5	245	2	Q89FJ8	Q89fj8 bradyrhizob	678	6	4.5	279	2	Q995A3	Q995a3 human herpe
606	6	4.5	246	2	Q97Y39	Q97y39 sulfolobus	679	6	4.5	279	2	Q995B6	Q995b6 human herpe
607	6	4.5	246	2	Q80W00	Q80w00 mus musculus	680	6	4.5	280	1	KD11_BACTN	Q8a284 bacteroides
608	6	4.5	247	2	Q970F9	Q970f9 sulfolobus	681	6	4.5	280	2	Q650K4	Q650k4 bacteroides
609	6	4.5	247	2	Q7QC8B	Q7qcb8 anopheles g	682	6	4.5	281	2	Q7WRR4	Q7wrr4 bartonella
610	6	4.5	247	2	Q6D1F6	Q6dlf6 erwinia car	683	6	4.5	281	2	Q7X255	Q7x255 bartonella
611	6	4.5	247	2	Q6G972	Q6g972 staphylococ	684	6	4.5	281	2	Q7X257	Q7x257 bartonella
612	6	4.5	247	2	Q6GGK6	Q6ggk6 staphylococ	685	6	4.5	281	2	Q7X261	Q7x261 bartonella
613	6	4.5	248	2	Q9VPM0	Q9vpm0 drosophila	686	6	4.5	282	2	Q7UGW3	Q7ugw3 rhodopirell
614	6	4.5	249	2	Q67X43	Q67x43 oryza sativ	687	6	4.5	283	2	Q64DP8	Q64dp8 uncultured
615	6	4.5	249	2	Q33598	Q33598 streptococc	688	6	4.5	283	2	Q67681	Q67681 aquifex aeo

689	6	4.5	283	2	Q83BH3	Q83bh3 coxiella bu	762	6	4.5	308	2	Q6CKS1	Q6cksl kluyveromyc
690	6	4.5	284	1	PURU_SYNV3	Q55135 synectocyst	763	6	4.5	308	2	Q7RNJ9	Q7rnj9 plasmodium
691	6	4.5	284	2	Q8LBY7	Q8lby7 arabidopsis	764	6	4.5	308	2	Q8DYR9	Q8dyr9 streptococc
692	6	4.5	284	2	Q8LW57	Q8lw57 arabidopsis	765	6	4.5	308	2	Q68EQ7	Q68eq7 xenopus tro
693	6	4.5	284	2	O10617	O10617 helicoverpa	766	6	4.5	308	2	Q6GP78	Q6gp78 xenopus lae
694	6	4.5	284	2	Q91BY8	Q91by8 helicoverpa	767	6	4.5	308	2	Q7SZT8	Q7sz8 xenopus lae
695	6	4.5	284	2	Q77L23	Q77l23 helicoverpa	768	6	4.5	308	2	Q7T390	Q7t390 brachydanio
696	6	4.5	284	2	Q801F0	Q801f0 xenopus lae	769	6	4.5	309	1	O4CD_HUMAN	Q8ngp0 homo sapien
697	6	4.5	285	2	Q6MX93	Q6mx93 azoarcus sp	770	6	4.5	309	1	PYRB_OCEIH	Q8er38 oceanobacil
698	6	4.5	286	2	O81013	O81013 arabidopsis	771	6	4.5	309	2	Q6XYV9	Q6xyv9 spioplasma
699	6	4.5	286	2	Q748Q2	Q748q2 geobacter s	772	6	4.5	310	2	Q97UW5	Q97uw5 sulfobolus
700	6	4.5	286	2	Q7NR69	Q7nr69 chromobacte	773	6	4.5	310	2	Q94961	Q94961 drosophila
701	6	4.5	289	2	Q9DSF1	Q9dsf1 human herpe	774	6	4.5	311	2	Q9CLL6	Q9cll6 pasteurella
702	6	4.5	290	1	Y283_METUA	Q57731 methanococc	775	6	4.5	312	2	Q8NH20	Q8nh20 homo sapien
703	6	4.5	290	2	Q8L7C1	Q8l7c1 arabidopsis	776	6	4.5	312	2	Q94912	Q94912 drosophila
704	6	4.5	290	2	Q84WH6	Q84wh6 arabidopsis	777	6	4.5	312	2	Q9LK86	Q9lk86 arabidopsis
705	6	4.5	290	2	Q74CA5	Q74ca5 geobacter s	778	6	4.5	312	2	Q7TQV2	Q7tqv2 mus musculu
706	6	4.5	290	2	Q88C26	Q88c26 pseudomonas	779	6	4.5	313	1	SURA_HAEIN	R44721 haemophilus
707	6	4.5	290	2	Q9DSF2	Q9dsf2 human herpe	780	6	4.5	313	2	Q81FJ5	Q81fj5 drosophila
708	6	4.5	290	2	Q6F8A9	Q6f8a9 xenopus tro	781	6	4.5	313	2	Q9CAZ0	Q9caz0 arabidopsis
709	6	4.5	291	2	Q6ZBX9	Q6zbx9 oryza sativ	782	6	4.5	313	2	Q84FM7	Q84fm7 thermus aqu
710	6	4.5	291	2	Q9LX76	Q9lx76 arabidopsis	783	6	4.5	313	2	Q6MIP2	Q6mip2 bdellovibri
711	6	4.5	292	1	SDHA_PEPAS	P33073 peptostrept	784	6	4.5	314	2	Q7RSR0	Q7rsr0 plasmodium
712	6	4.5	293	2	Q7WVW5	Q7wvw5 streptococc	785	6	4.5	314	2	O6LGV3	O6lqv3 photobacter
713	6	4.5	293	2	Q745V5	Q745v5 thermus the	786	6	4.5	315	2	Q6FLH6	Q6flh6 candida gla
714	6	4.5	293	2	Q7TTH4	Q7ttw4 synectococc	787	6	4.5	315	2	Q9SCQ1	Q9scq1 arabidopsis
715	6	4.5	293	2	Q9CWN2	Q9cwn2 mus musculu	788	6	4.5	315	2	Q9JWC1	Q9jwc1 neisseria m
716	6	4.5	293	2	Q6UED8	Q6ued8 xenopus lae	789	6	4.5	316	2	Q9M2H6	Q9m2h6 arabidopsis
717	6	4.5	294	1	VU51_HHVJ7	P52383 human herpe	790	6	4.5	317	2	Q96B32	Q96b32 homo sapien
718	6	4.5	294	2	Q834B2	Q834b2 enterococcu	791	6	4.5	317	2	O65KX5	O65kx5 bacillus li
719	6	4.5	294	2	Q77Y65	Q77y65 human herpe	792	6	4.5	318	2	O06829	O06829 mycobacteri
720	6	4.5	295	2	Q68QJ4	Q68qf4 lithobius f	793	6	4.5	318	2	O53795	O53795 mycobacteri
721	6	4.5	295	2	Q9SJD3	Q9sjd3 arabidopsis	794	6	4.5	318	2	Q7D9D6	Q7d9d6 mycobacteri
722	6	4.5	295	2	O83587	O83587 treponema p	795	6	4.5	318	2	Q7UI85	Q7ui85 mycobacteri
723	6	4.5	295	2	Q7MTI9	Q7mti9 porphyromon	796	6	4.5	319	1	YC39_PORPU	P51238 porphyra pu
724	6	4.5	296	2	Q7V1O3	Q7v1o3 prochloroco	797	6	4.5	319	2	O8VR33	O8vfr33 mus musculu
725	6	4.5	296	2	Q7W634	Q7w634 bordetella	798	6	4.5	319	2	Q9DGM0	Q9dgm0 gallus gall
726	6	4.5	296	2	Q7W100	Q7w100 bordetella	799	6	4.5	320	1	CY11_SOLTU	P25076 solanum tub
727	6	4.5	296	2	Q66KB7	Q66ke7 xenopus lae	800	6	4.5	320	2	O855I5	O855i5 mycobacteri
728	6	4.5	297	1	FTR_METBA	P55301 methanosarc	801	6	4.5	320	2	Q41207	Q41207 solanum tub
729	6	4.5	297	2	Q7M819	Q7m819 wolinnella s	802	6	4.5	320	2	O8XI86	O8xi86 clostridium
730	6	4.5	298	1	OCRC_AGRTU	O00679 agrobacteri	803	6	4.5	320	2	O8XVQ6	O8xvq6 ralstonia s
731	6	4.5	298	2	Q9SLX1	Q9slx1 arabidopsis	804	6	4.5	321	1	TRYC_HUMAN	Q9nrz2 homo sapien
732	6	4.5	299	2	Q97U89	Q97u89 sulfobolus	805	6	4.5	321	2	Q96RZ8	Q96rr8 homo sapien
733	6	4.5	299	2	Q89YF2	Q89yf2 bacteroides	806	6	4.5	321	2	Q67NQ4	Q67mq4 symbiobacte
734	6	4.5	300	2	Q65KU9	Q65ku9 bacillus li	807	6	4.5	321	2	Q6NEJ5	Q6njb5 rhodopseudo
735	6	4.5	300	2	O34990	O34990 bacillus su	808	6	4.5	321	2	Q7N6Y0	Q7n6y0 photorhabdu
736	6	4.5	300	2	O88E64	O88e64 pseudomonas	809	6	4.5	322	2	O8NSY8	O8nsy8 homo sapien
737	6	4.5	300	2	Q9HXB6	Q9hxb6 pseudomonas	810	6	4.5	322	2	Q8UJU0	Q8uju0 agrobacteri
738	6	4.5	301	1	Y186_MYCPN	P75265 mycoplasma	811	6	4.5	322	2	O8YY66	O8yy66 anabaena sp
739	6	4.5	301	2	Q8WEY3	Q8wey3 septifer vi	812	6	4.5	322	2	O8G2V1	O8g2v1 bruceella su
740	6	4.5	301	2	Q67Z40	Q67z40 arabidopsis	813	6	4.5	322	2	Q8CC71	Q8cc71 mus musculu
741	6	4.5	301	2	Q82F88	Q82f88 streptomyce	814	6	4.5	322	2	Q7TMM8	Q7tm8 mus musculu
742	6	4.5	301	2	O91BU8	O91bu8 helicoverpa	815	6	4.5	323	2	O6PK64	O6pk64 homo sapien
743	6	4.5	301	2	Q77LW4	Q77lw4 helicoverpa	816	6	4.5	324	2	Q758I8	Q758i8 ashbya goss
744	6	4.5	301	2	Q9E225	Q9e225 helicoverpa	817	6	4.5	324	2	Q9UXL0	Q9jxi0 neisseria m
745	6	4.5	302	2	Q9C4R6	Q9c4r6 methanosarc	818	6	4.5	325	2	O95W95	O95w95 crithidia f
746	6	4.5	302	2	Q6BQK3	Q6bqk3 debaryomyce	819	6	4.5	325	2	O630A6	O630a6 bacillus li
747	6	4.5	302	2	Q7TUV8	Q7tuv8 prochloroco	820	6	4.5	325	2	O65PL5	O65pl5 bacillus li
748	6	4.5	303	2	P87589	P87589 citrus tris	821	6	4.5	325	2	Q7VCH0	Q7vch0 prochloroco
749	6	4.5	304	2	O942X6	O942x6 oryza sativ	822	6	4.5	326	1	DED2_HUMAN	O8wxr8 homo sapien
750	6	4.5	304	2	O66991	O66991 aquifex aeo	823	6	4.5	326	2	Q9KWR0	Q9kwr0 bacillus sp
751	6	4.5	304	2	Q7UY63	Q7uy63 rhodospirell	824	6	4.5	327	2	Q7NNM39	Q7nm39 gloeobacter
752	6	4.5	305	2	Q7Q874	Q7q874 anopheles g	825	6	4.5	327	2	O89NF9	O89nf9 bradyrhizob
753	6	4.5	305	2	O67885	O67885 aquifex aeo	826	6	4.5	327	2	Q8D2M7	Q8d2m7 wigglewort
754	6	4.5	306	2	O86SN0	O86sn0 homo sapien	827	6	4.5	327	2	O8I131	O8i131 human herpe
755	6	4.5	307	1	YL72_ARCFU	Q28110 archaeoglob	828	6	4.5	327	2	Q7ZTA1	Q7zta1 brachydanio
756	6	4.5	307	2	Q94962	Q94962 drosophila	829	6	4.5	329	2	Q8U8N0	Q8u8n0 agrobacteri
757	6	4.5	307	2	Q8NT50	Q8nte0 corynebacte	830	6	4.5	330	1	DED2_MOUSE	O8qzv0 mus musculu
758	6	4.5	307	2	G6PC34	G6pc34 brachydanio	831	6	4.5	330	2	O6EGR7	O6egr7 gonatocerus
759	6	4.5	308	1	GSN2_HUMAN	Q9nz01 homo sapien	832	6	4.5	330	2	Q858T2	Q858t2 bacterioph
760	6	4.5	308	1	GSN2_MOUSE	Q9cy27 mus musculu	833	6	4.5	330	2	Q7V2N4	Q7v2n4 prochloroco
761	6	4.5	308	1	GSN2_RAT	Q64232 rattus norv	834	6	4.5	331	2	Q6NB10	Q6nb10 rhodopseudo

Q6cksl kluyveromyc	Q7rnj9 plasmodium	Q8dyr9 streptococc	Q68eq7 xenopus tro	Q6gp78 xenopus lae	Q7sz8 xenopus lae	Q7t390 brachydanio	Q8ngp0 homo sapien	Q8er38 oceanobacil	Q6xyv9 spioplasma	Q97uw5 sulfobolus	Q94961 drosophila	Q9cll6 pasteurella	Q8nh20 homo sapien	Q94912 drosophila	Q9lk86 arabidopsis	Q7tqv2 mus musculu	R44721 haemophilus	Q81fj5 drosophila	Q9caz0 arabidopsis	Q84fm7 thermus aqu	Q6mip2 bdellovibri	Q7rsr0 plasmodium	O6lqv3 photobacter	Q6flh6 candida gla	Q9scq1 arabidopsis	Q9jwc1 neisseria m	Q9m2h6 arabidopsis	Q96b32 homo sapien	O65kx5 bacillus li	O06829 mycobacteri	O53795 mycobacteri	Q7d9d6 mycobacteri	Q7ui85 mycobacteri	P51238 porphyra pu	O8vfr33 mus musculu	Q9dgm0 gallus gall	P25076 solanum tub	O855i5 mycobacteri	Q41207 solanum tub	O8xi86 clostridium	O8xvq6 ralstonia s	Q9nrz2 homo sapien	Q96rr8 homo sapien	Q67mq4 symbiobacte	O6njb5 rhodopseudo	Q7n6y0 photorhabdu	O8nsy8 homo sapien	Q8uju0 agrobacteri	O8yy66 anabaena sp	O8g2v1 bruceella su	O8cc71 mus musculu	Q7tm8 mus musculu	O6pk64 homo sapien	Q758i8 ashbya goss	Q9jxi0 neisseria m	O95w95 crithidia f	O630a6 bacillus li	O65pl5 bacillus li	Q7vch0 prochloroco	O8wxr8 homo sapien	Q9kwr0 bacillus sp	Q7nm39 gloeobacter	O89nf9 bradyrhizob	Q8d2m7 wigglewort	O8i131 human herpe	Q7zta1 brachydanio	Q8u8n0 agrobacteri	O8qzv0 mus musculu	O6egr7 gonatocerus	Q858t2 bacterioph	Q7v2n4 prochloroco	Q6nb10 rhodopseudo
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835	6	4.5	331	2	Q7VDX4	Q7vdx4 prochloroco	908	2	Q6PIA3	Q6pia3 homo sapien
836	6	4.5	331	2	Q6IRJ6	Q6irj6 rattus norv	909	2	Q8I2L3	Q8i2l3 plasmodium
837	6	4.5	331	2	Q6JL55	Q6jl55 rattus norv	910	2	Q8PJJC3	Q8pjjc3 xanthomonas
838	6	4.5	332	2	Q759U4	Q759u4 aebhya goss	911	2	Q8XNA0	Q8xna0 clostridium
839	6	4.5	332	2	Q71S47	Q71s47 ophiopholis	912	2	Q8C0J3	Q8c0j3 yarrowia li
840	6	4.5	332	2	Q97QC7	Q97qc7 streptococc	913	2	Q966A1	Q966a1 caenorhabdi
841	6	4.5	332	2	Q7V372	Q7v372 prochloroco	914	2	Q6H742	Q6h742 oryza sativ
842	6	4.5	333	2	Q8PM92	Q8pm92 xanthomonas	915	2	Q6JZA7	Q6jza7 escherichia
843	6	4.5	333	2	Q87FK6	Q87fk6 vibrio para	916	2	Q6JZB1	Q6jzb1 escherichia
844	6	4.5	334	1	ALG5_YEAST	P40350 saccharomyc	917	2	Q9NG28	Q9ng28 planotortri
845	6	4.5	334	1	Y472_RICPR	Q9zd72 rickettsia	918	2	Q87J69	Q87j69 vibrio para
846	6	4.5	334	2	O14125	O14125 schizosacch	919	2	Q8V5T6	Q8v5t6 helicoverpa
847	6	4.5	334	2	Q6VPL9	Q6vpl9 salmonella	920	2	FUS3_YEAST	P16892 saccharomyc
848	6	4.5	334	2	Q6F1R6	Q6f1r6 mesoplasma	921	2	Q94G17	Q94g17 pisum sativ
849	6	4.5	335	2	Q8TML1	Q8tml1 methanosarc	922	2	Q6JZA8	Q6jza8 escherichia
850	6	4.5	335	2	Q9PLP4	Q9plp4 chlamydia m	923	2	Q6JZB4	Q6jzb4 escherichia
851	6	4.5	336	2	Q8ZNF1	Q8znf1 homo sapien	924	2	Q6JZC0	Q6jzc0 escherichia
852	6	4.5	336	2	Q8GHA9	Q8gha9 streptomyce	925	2	Q6JZD3	Q6jzd3 escherichia
853	6	4.5	336	2	Q9F8T0	Q9f8t0 streptomyce	926	2	Q6JZD4	Q6jzd4 escherichia
854	6	4.5	336	2	Q72R03	Q72r03 leptospira	927	2	Q63I88	Q63i88 burkholderi
855	6	4.5	336	2	Q8F4T4	Q8f4t4 leptospira	928	2	Q65UX4	Q65ux4 manheimia
856	6	4.5	337	2	Q6ZQV3	Q6zqv3 homo sapien	929	2	RFL_THETH	P96077 thermus the
857	6	4.5	337	2	Q9N382	Q9n382 caenorhabdi	930	2	Q6JZD1	Q6jzd1 escherichia
858	6	4.5	337	2	Q7CTZ4	Q7ctz4 agrobacteri	931	2	Q6JZD2	Q6jzd2 escherichia
859	6	4.5	337	2	Q8CQ08	Q8cqu8 oceanobacil	932	2	Q72HB8	Q72hb8 thermus the
860	6	4.5	337	2	Q8DHQ2	Q8dhq2 synechococc	933	2	Q8e4f3	Q8e4f3 streptococc
861	6	4.5	337	2	Q8E211	Q8e211 carcopitheo	934	2	AROB_STRAS	AROB_STRAS3
862	6	4.5	338	2	Q8C582	Q8c582 yarrowia li	935	2	AROB_STRMU	AROB_STRMU
863	6	4.5	338	2	Q8LB09	Q8lb09 arabidopsis	936	2	AROB_STRPN	AROB_STRPN
864	6	4.5	338	2	Q8C9D0	Q8c9d0 arabidopsis	937	2	AROB_STRR6	AROB_STRR6
865	6	4.5	338	2	Q8XQ11	Q8xq11 ralsstonia s	938	2	Q8HDV5	Q8hdv5 carabus vig
866	6	4.5	338	2	Q9K5W3	Q9k5w3 bacillus ha	939	2	Q8HDV6	Q8hdv6 carabus vig
867	6	4.5	339	1	TRAI_COXBU	Q45968 coxiella bu	940	2	Q8HDV7	Q8hdv7 carabus vig
868	6	4.5	339	2	Q97Y21	Q97y21 sulfolobus	941	2	Q8HDV9	Q8hdv9 carabus lat
869	6	4.5	339	2	Q8FQC4	Q8fqc4 candida gia	942	2	Q8HDW0	Q8hdw0 carabus pee
870	6	4.5	339	2	Q9Z199	Q9zi99 lactobacill	943	2	Q8HDW3	Q8hdw3 carabus koi
871	6	4.5	339	2	Q8CX99	Q8cx99 oceanobacil	944	2	Q8HDW4	Q8hdw4 carabus par
872	6	4.5	339	2	Q70411	Q70411 rattus norv	945	2	Q8HDW5	Q8hdw5 carabus don
873	6	4.5	340	2	Q9XMP1	Q9xmp1 ceratitis c	946	2	Q8HDW6	Q8hdw6 carabus obl
874	6	4.5	340	2	Q6YCH1	Q6ych1 mus musculu	947	2	Q8HDW7	Q8hdw7 carabus yun
875	6	4.5	340	2	Q7ZV12	Q7zv12 brachydanio	948	2	Q8HDW8	Q8hdw8 carabus mor
876	6	4.5	341	2	Q8THW7	Q8thw7 methanosarc	949	2	Q8HDW9	Q8hdw9 carabus nes
877	6	4.5	341	2	Q9NB46	Q9nb46 caenorhabdi	950	2	Q8HDX0	Q8hdw0 carabus nan
878	6	4.5	341	2	Q95B78	Q95b78 gymnolaena	951	2	Q6JZA6	Q6jza6 escherichia
879	6	4.5	341	2	Q95B84	Q95b84 gymnolaena	952	2	AROB_CLOAB	AROB_CLOAB
880	6	4.5	341	2	Q95B85	Q95ba5 dysnodia pi	953	2	YDGC_SCHPO	YDGC_SCHPO
881	6	4.5	341	2	Q95BB2	Q95bb2 dysnodia pa	954	2	Q6JZD0	Q6jzd0 escherichia
882	6	4.5	341	2	Q95BB4	Q95bb4 boeberoides	955	2	Q84QU2	Q84qu2 oryza sativ
883	6	4.5	341	2	Q95B94	Q95b94 schizotrich	956	2	Q93IP4	Q93ip4 synechococc
884	6	4.5	341	2	Q8Y2Z0	Q8y2z0 brucella me	957	2	Q6JZB8	Q6jzb8 escherichia
885	6	4.5	341	2	Q8ES16	Q8es16 oceanobacil	958	2	Q7RDD9	Q7rdd9 plasmodium
886	6	4.5	341	2	Q80ZU1	Q80zul mus musculu	959	2	Q7P2Y8	Q7p2y8 fusobacteri
887	6	4.5	341	2	Q6GMG4	Q6gm94 brachydanio	960	2	Q7TDD5	Q7tdd5 tomato leaf
888	6	4.5	342	1	AN1H_HUMAN	P61962 homo sapien	961	2	Q9AVE6	Q9ave6 oryza sativ
889	6	4.5	342	1	AN1H_MOUSE	P61963 mus musculu	962	2	AROB_THEAC	AROB_THEAC
890	6	4.5	342	1	Q7R4G3	Q7r4g3 giardia lam	963	2	REC_F_SHEON	REC_F_SHEON
891	6	4.5	342	2	Q65Q84	Q65q84 manheimia	964	2	Q97ZL1	Q97zl1 sulfolobus
892	6	4.5	342	2	Q8F648	Q8f648 xenopus tro	965	2	Q96CC2	Q96cc2 homo sapien
893	6	4.5	342	2	Q7ZY00	Q7zy00 xenopus lae	966	2	Q6JZA9	Q6jza9 escherichia
894	6	4.5	343	2	Q95B94	Q95b94 schizotrich	967	2	Q9F3K1	Q9f3k1 streptomyce
895	6	4.5	343	2	Q7ZY56	Q7zy56 xenopus lae	968	2	Q9C899	Q9c899 arabidopsis
896	6	4.5	344	2	Q8WY52	Q8wy52 homo sapien	969	2	Q9LHN8	Q9lhn8 arabidopsis
897	6	4.5	344	2	Q73MW5	Q73mw5 treponema d	970	2	Q7MAW9	Q7maw9 porphyronon
898	6	4.5	345	2	Q86403	Q86403 methanobact	971	2	Q7UGV3	Q7ugv3 rhodopirell
899	6	4.5	345	2	Q8XL96	Q8xl96 clostridium	972	2	Q8FBR9	Q8fbr9 escherichia
900	6	4.5	346	2	Q65M77	Q65m77 bacillus li	973	2	Q8JZ15	Q8jz15 tomato leaf
901	6	4.5	347	2	Q697K7	Q697k7 aulacoseira	974	2	Q80A85	Q80a85 tomato leaf
902	6	4.5	347	2	Q6JZA5	Q6jza5 escherichia	975	2	REC_F_PROMI	REC_F_PROMI
903	6	4.5	348	1	MER_METKA	Q8txy4 methanopyru	976	2	Q820W2	Q820w2 coxiella bu
904	6	4.5	348	2	Q9TD13	Q9tdl3 maratecoara	977	2	Q9FGH5	Q9fgh5 arabidopsis
905	6	4.5	348	2	Q9TD13	Q9tdl3 maratecoara	978	2	Q67NT4	Q67nt4 symbiobacte
906	6	4.5	349	2	Q704B5	Q704b5 thermoprote	979	2	Q9F720	Q9f720 chlorobium
907	6	4.5	349	2	Q6CUD6	Q6cuu6 kluyveromyc	980	2	Q6P207	Q6p207 mus musculu


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DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
KW Antigen; Nuclear protein.
FT DOMAIN 31 161
FT DOMAIN 71 191
FT DOMAIN 173 297
FT SEQUENCE 374 AA; 42132 MW; EE5F4C5CF6FD09DC CRC64;
Query Match 100.0%; Score 132; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 9.6e-131;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFCREEMGEVTKSTPSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 60
Db 33 SYMTINNFCREEMGEVTKSTPSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 92
Qy 61 CPKSEVRKFKFSILNAKGETKAMESQRAYRFVQGDWPKFKFIRRDFLDEANGLLPD 120
Db 93 CPKSEVRKFKFSILNAKGETKAMESQRAYRFVQGDWPKFKFIRRDFLDEANGLLPD 152
Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164
RESULT 3
SPOP MOUSE
ID -SPOP MOUSE STANDARD; PRT; 374 AA.
AC Q6ZNS8;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Speckle-type POZ protein (PDX-1 C-terminal interacting factor 1)
DE (PCIF1).
GN Name=Spop; Synonyms=Pcif1;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, AND INTERACTION
WITH IPF1/PDX1.
RC STRAIN=BALB/c; TISSUE=Pancreas;
RX PubMed=15121856; DOI=10.1128/MCB.24.10.4372-4383.2004;
RA Liu A., Desai B.M., Stoffers D.A.;
"Identification of PCIF1, a POZ domain protein that inhibits PDX-1
(MODY4) transcriptional activity.";
RL Mol. Cell. Biol. 24:4372-4383(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Oeato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarrelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
Blake J.A., Bradt D., Brusci V., Chothia C., Corbani L.E., Cousins S.,
Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
Gratmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
Kanai A., Kawaji H., Kawasaki Y., Kiedziarski R.M., King B.L.,
Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
Nagashima T., Nunata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
Sandelin A., Schneider C., Sempke C.A., Setou M., Shimada K.,
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RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
Wilming L.G., Wynehaw-Boriss A., Yanagisawa M., Yang I., Yang L.,
Yuan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
Birney E., Hayashizaki Y.;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
CC -!- FUNCTION: Inhibits IPF1/PDX1 transactivation of established target
promoters, such as insulin, may be by recruiting a repressor
complex.
CC -!- SUBUNIT: Interacts with IPF1/PDX1.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- TISSUE SPECIFICITY: Widely expressed, mainly in pancreas and in
particular in adult pancreatic insulin-producing beta cells and in
a subset of exocrine acinar and duct cells.
CC -!- SIMILARITY: Contains 1 BTB/POZ domain.
CC -!- SIMILARITY: Contains 1 MATH domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@sib-sib.ch).
DR EMBL; AY538613; AAT08952.1; -
DR EMBL; AK030746; BAC27114.1; -
DR EMBL; AK028201; BAC25809.1; -
DR InterPro; IPR00210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
KW Nuclear protein.
FT DOMAIN 31 161
FT DOMAIN 71 191
FT SEQUENCE 374 AA; 42132 MW; EE5F4C5CF6FD09DC CRC64;
Query Match 100.0%; Score 132; DB 1; Length 374;
Best Local Similarity 100.0%; Pred. No. 9.6e-131;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SYMTINNFCREEMGEVTKSTPSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 60
Db 33 SYMTINNFCREEMGEVTKSTPSSGANDKLKWLVRNPKGLDESKDYLSTLLVLS 92
Qy 61 CPKSEVRKFKFSILNAKGETKAMESQRAYRFVQGDWPKFKFIRRDFLDEANGLLPD 120
Db 93 CPKSEVRKFKFSILNAKGETKAMESQRAYRFVQGDWPKFKFIRRDFLDEANGLLPD 152
Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164
RESULT 4
Q6P8B3
ID Q6P8B3
AC Q6P8B3;
PRT; 374 AA.
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DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MGC75799.
GN Name=MGC75799;
OS Xenopus tropicalis (western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=83364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whitling M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Gerhards D.S.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
EMBL: BC061316; AAH61316.1; -.
GO: GO:0005515; F:protein binding; IEA.
DR InterPro; IPR00210; BTF_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTF; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00061; MATH; 1.
DR SMART; SM00225; BTF; 1.
DR PROSITE; PS50097; BTF; 1.
DR PROSITE; PS50144; MATH; 1.
KW Hypothetical protein.
SQ SEQUENCE 374 AA; 42154 MW; 2DC5738B57025BF7 CRC64;

Query Match 100.0%; Score 132; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 9.6e-131;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMMTINNFSFCREEMGEVIKSTFFSGANDKLKWLCLRVNPKGLDEESKDYLISLYLLVS 60
Db 33 SYMMTINNFSFCREEMGEVIKSTFFSGANDKLKWLCLRVNPKGLDEESKDYLISLYLLVS 92

Qy 61 CPKSEVRAPKFSILNAKGETKAMESQRAYRFVQKDWGFKKFIIRDRLDDEANGLLPD 120
Db 93 CPKSEVRAPKFSILNAKGETKAMESQRAYRFVQKDWGFKKFIIRDRLDDEANGLLPD 152

Qy 121 DKLTLCFCEVSV 132
Db 153 DKLTLCFCEVSV 164

RESULT 5
Q7T330 PRELIMINARY; PRT; 374 AA.
ID Q7T330
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Q7ZX06 PRELIMINARY; PRT; 374 AA.
Q7ZX06; 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE C9924-prov protein.
GN Name=c9924-prov;
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN RFL
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins C.M., Wagner L., Shenmen G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Schmutz J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative";
RL Dev. Dyn. 225:384-391 (2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC046272; AAA46272.1; ~
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR002010; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS01044; MATH; 1.
SQ SEQUENCE 374 AA; 42154 MW; 2DC5738E57025BF7 CRC64;
Query Match 100.0%; Score 132; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 9.6e-131; Gaps 0;
Matches 132; Conservative 0; Mismatches 0; Indels 0;
QY 1 SYMTINNFSFCREEMGEVIVKSTPSSGANDKWKCLRVNPKGLDEESKDYLSLYLLVS 60
DB 33 SYMTINNFSFCREEMGEVIVKSTPSSGANDKWKCLRVNPKGLDEESKDYLSLYLLVS 92
QY 61 CPKSEVRKFKPSILNAKEETKAMESQRAVRFVQKDWGPKFKFTRRDFLLDEANGLLPD 120
DB 93 CPKSEVRKFKPSILNAKEETKAMESQRAVRFVQKDWGPKFKFTRRDFLLDEANGLLPD 152

QY 121 DKLTFLFCEVSVV 132
DB 153 DKLTFLFCEVSVV 164
RESULT 7
Q9DBZ2 PRELIMINARY; PRT; 425 AA.
AC Q9DBZ2; 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mus musculus adult male lung cDNA, RIKEN full-length enriched library,
DE clone:1200009E17 product:speckle-type POZ protein, full insert
DE sequence.
GN Name=Spop;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN RFL
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-3;
RA Carninci P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning";
RL Meth. Enzymol. 303:19-44 (1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection";
RL Nature 409:685-690 (2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes";
RL Genome Res. 10:1617-1630 (2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kasniwagi K.,
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multipipette sequencer";
RL Genome Res. 10:1757-1771 (2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Lung;
RX Adachi J., Aizawa K., Akabira S., Akimura T., Arai A., Aono H.,
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Horii F.,
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,

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RA Mateuyama T., Miyazaki A., Nishi K., Nomura K., Nomura K., Numazaki R., Ohno M.,
RA Okazaki Y., Okido T., Owa C., Saito K., Saito R., Sakai C., Sakai K.,
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
RA Muramatsu M., Hayaishizaki Y.,
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK004669; BAB23458.1; -.
DR MGD; MGI:1343085; Spop.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS00144; MATH; 1.
DR PROSITE; PS00144; MATH; 1.
SQ SEQUENCE 425 AA; 47514 MW; 7B6716666C3D884B CRC64;

Query Match 100.0%; Score 132; DB 2; Length 425;
Best Local Similarity 100.0%; Pred. No. 1.1e-130;
Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SYMTINNFSRCREMGVIVKSSFTSSGANDKLKWLKLVNPKGLDERSKDYLSLYLLVLS 60
Db 33 SYMTINNFSRCREMGVIVKSSFTSSGANDKLKWLKLVNPKGLDERSKDYLSLYLLVLS 92

Qy 61 CPKSEVRKPFSLINAKGETKAMESORAYRVQGDWGFKKFIRDRFLDDEANGLLPD 120
Db 93 CPKSEVRKPFSLINAKGETKAMESORAYRVQGDWGFKKFIRDRFLDDEANGLLPD 152

Qy 121 DKLTLCFCEVSVV 132
Db 153 DKLTLCFCEVSVV 164

RESULT 8
Q9HAB2
ID Q9HAB2 PRELIMINARY; PRT; 391 AA.
AC Q9HAB2;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein FLJ11857.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole embryo;
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura T., Makita H.,
RA Sekine M., Oobayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto K., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahara K.,
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,
RA Sudo H., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,
RA Tanai H., Kinata M., Watanabe M., Hiraoa S., Chiba Y., Ishida S.,
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
RA Mueshino K., Yuuki H., Ohshima A., Sasaki N., Aotsuka S.,
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
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RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
RA Kawabata A., Hikiji T., Kobatake N., Itagaki H., Ikema Y., Okamoto S.,
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isegai T., Sugano S.;
RT "Complete sequencing and characterization of 21,243 full-length human
RT cDNAs.";
RL Nat. Genet. 36:40-45(2004).
DR EMBL; AK021919; BAB13937.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS00097; BTB; 1.
DR PROSITE; PS00144; MATH; 1.
DR PROSITE; PS00144; MATH; 1.
SQ SEQUENCE 391 AA; 44874 MW; 90DC2449E9141FD7 CRC64;

Query Match 40.2%; Score 53; DB 2; Length 391;
Best Local Similarity 100.0%; Pred. No. 3.7e-47;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRVQGDWGFKKFIRDRFLDDEANGLLPDKLTLCFCEVSVV 132
Db 112 EETKAMESQRAYRVQGDWGFKKFIRDRFLDDEANGLLPDKLTLCFCEVSVV 164

RESULT 9
Q6IQ16
ID Q6IQ16 PRELIMINARY; PRT; 392 AA.
AC Q6IQ16;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein LOC339745.
GN Name=LOC339745;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Dratchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield V.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC TISSUE=Brain;
RA Strausberg R.;
RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC071613; AAH71613.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
KW Hypothetical protein.
SQ
SEQUENCE 392 AA; 44647 MW; CEB4243BD732DFEF CRC64;

Query Match 40.2%; Score 53; DB 2; Length 392;
Best Local Similarity 100.0%; Pred. No. 3.7e-47;
Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPDDKLTFLFCEVSW 132
Db 112 EETKAMESQRAYRFVQGDWGFKKFIRDFLLDEANGLLPDDKLTFLFCEVSW 164

RESULT 10
Q8MRB4 PRELIMINARY; PRT; 374 AA.
AC Q8MRB4; Q9VFP3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE E34508P (CG9924-PB).
GN ORFNames=CG9924;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R.A., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RA Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Frannkoc C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Fowler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasco P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY121682; AAM52009.1; -.
DR EMBL; AE003702; AAN14348.1; -.
DR IntAct; Q8MRB4; -.
DR FlyBase; Fgn0038192; CG9924.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB_POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.

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DR PROSITE: PS50144; MATH: 1.
SQ SEQUENCE 374 AA; 4283 MW; 2116548EB64F04C0 CRC64;

Query Match 30.3%; Score 40; DB 2; Length 374;
Best Local Similarity 100.0%; Pred. No. 2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 119
Db 112 EETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 151

RESULT 11

Q7PGC0 PRELIMINARY; PRT; 401 AA.

AC Q7PGC0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000024127 (Fragment).
GN Name=ENSANGG0000011135;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AA0801008951; EAA44989.1; -.
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR002010; BTF POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTF; 1.
DR Pfam; PF00917; MATH; 1.
DR PROSITE; PS50097; BTF; 1.
DR PROSITE; PS50144; MATH; 1.
FT NON TER 1
SQ SEQUENCE 401 AA; 45025 MW; 7769BDAC20DFB86 CRC64;

Query Match 30.3%; Score 40; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.2e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 119
Db 139 EETKAMESQRAYRFVQKDWGFKFKFIRDFLLDEANGLLP 178

RESULT 12

Q8ING4 PRELIMINARY; PRT; 403 AA.

AC Q8ING4;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG9924-PC (CG9924-pd) (RE74593p).
GN ORFNames=CG9924;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt C., Nelson C.R., Gabor G.L.,
Abril J.F., Agbayani A., An H.J., Andrews-Pfankoch C., Baldwin D.,
Ballew R.M., Basu A., Bakendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
Fosler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam K.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zhu S.,
Zhong F.N., Zhong W., Zhou X., Zhou S., Zhu X., Smith H.O.,
Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
[2]
SEQUENCE FROM N.A.
MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
"Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
[3]
SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
Ashburner M., Celniker S.E.;
"The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
[4]
SEQUENCE FROM N.A.
MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
Lewis S.E.;
"Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
[5]
SEQUENCE FROM N.A.
FlyBase;

Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6] SEQUENCE FROM N.A.
 RA FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 [7] SEQUENCE FROM N.A.
 RP STRAIN=Berkeley;
 RA Stapleton M., Carlson J., Chavez C., Frise E., George R., Pacleb J.,
 RA Park S., Wan K., Yu C., Rubin G.M., Celniker S.;
 RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB003702; AAN14346.1; -;
 DR EMBL; BT012443; AAS93714.1; -;
 DR FlyBase; FBgn0038192; CG9924.
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR002083; MATH.
 DR InterPro; IPR008974; Traf_like.
 DR Pfam; PF00651; BTB; 1.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00061; MATH; 1.
 DR PROSITE; PS50097; BTB; 1.
 DR PROSITE; PS50144; MATH; 1.
 SQ SEQUENCE 403 AA; 45310 MW; 190BB5EC3B108CD8 CRC64;
 Query Match 30.3%; Score 40; DB 2; Length 403;
 Best Local Similarity 100.0%; Pred. No. 2.2e-33;
 Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 80 EETKAMESQRAYRFVQGWGFKFIRDFLLDEANGLLP 119
 DB 141 EETKAMESQRAYRFVQGWGFKFIRDFLLDEANGLLP 180
 RESULT 13
 Q7KSK6
 ID Q7KSK6 PRELIMINARY; PRT; 406 AA.
 AC Q7KSK6
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE CG9924-PA.
 GN ORFNames=CG9924;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.R., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Frankoch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieria S., Fleischmann W.,
 RA Fodor C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Hostin N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hootin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

LAASKO P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Massarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6] SEQUENCE FROM N.A.
 RP FlyBase;
 RG Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RL EMBL; AB003702; AAF55007.3; -;
 DR GO; GO:0005515; F:protein binding; IEA.
 DR InterPro; IPR000210; BTB_POZ.
 DR InterPro; IPR002083; MATH.
 DR InterPro; IPR008974; Traf_like.
 DR Pfam; PF00651; BTB; 1.
 DR Pfam; PF00917; MATH; 1.
 DR SMART; SM00225; BTB; 1.
 DR SMART; SM00061; MATH; 1.
 DR PROSITE; PS50097; BTB; 1.
 DR PROSITE; PS50144; MATH; 1.
 SQ SEQUENCE 406 AA; 45750 MW; 344A5EA7A271D404 CRC64;
 Query Match 30.3%; Score 40; DB 2; Length 406;

Best Local Similarity 100.0%; Pred. No. 2.2e-33; Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGDWGFKKFIRRDFFLLDEANGLLP 119
|||||
Db 144 BETKAMESQRAYRFVQGDWGFKKFIRRDFFLLDEANGLLP 183
|||||

RESULT 14

YNVS CAEEL STANDARD; PRT; 451 AA.
AC P34568;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein T16H12.5 in chromosome III.
GN ORFNames=T16H12.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology."
RL Science 282:2012-2018(1998).
RN [2]

RP REVISIONS.

RA Durbin R.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Contains 1 BTB/POZ domain.
CC -1- SIMILARITY: Contains 1 MATH domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See [http://www.isb-sib.ch/](http://www.isb-sib.ch/announce/)
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; Z30662; CAA83138.2; -
DR WormBase; WBGene0011815; T16H12.5.
DR WormPep; T16H12.5; CE29054.
DR InterPro; IPR000210; BTB POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR SMART; SM00225; BTB; 1.
DR SMART; SM00061; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
KW Hypothetical protein.
FT DOMAIN 95 225 MATH.
FT DOMAIN 265 338 BTB.
SQ SEQUENCE 451 AA; 51062 MW; B36B1C618FBBB3A3 CRC64;

Query Match 30.3%; Score 40; DB 1; Length 451;
Best Local Similarity 100.0%; Pred. No. 2.4e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGDWGFKKFIRRDFFLLDEANGLLP 119
|||||
Db 176 BETKAMESQRAYRFVQGDWGFKKFIRRDFFLLDEANGLLP 215
|||||

RESULT 15

Q7PRD7
ID Q7PRD7 PRELIMINARY; PRT; 695 AA.

AC Q7PRD7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ENSANGP0000013624 (Fragment).
GN Name=ENSANGG0000011135;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01008851; EAA07408.2; -
DR GO; GO:0005515; F:protein binding; IEA.
DR InterPro; IPR000210; BTB POZ.
DR InterPro; IPR002083; MATH.
DR InterPro; IPR008974; Traf_like.
DR Pfam; PF00651; BTB; 1.
DR Pfam; PF00917; MATH; 1.
DR PROSITE; PS50097; BTB; 1.
DR PROSITE; PS50144; MATH; 1.
FT NON TER 695 695
SQ SEQUENCE 695 AA; 72892 MW; 95934611BB34BDAA CRC64;

Query Match 30.3%; Score 40; DB 2; Length 695;
Best Local Similarity 100.0%; Pred. No. 3.5e-33;
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 EETKAMESQRAYRFVQGDWGFKKFIRRDFFLLDEANGLLP 119
|||||
Db 112 EETKAMESQRAYRFVQGDWGFKKFIRRDFFLLDEANGLLP 151
|||||

Search completed: July 20, 2005, 20:52:15
Job time : 119.8 secs